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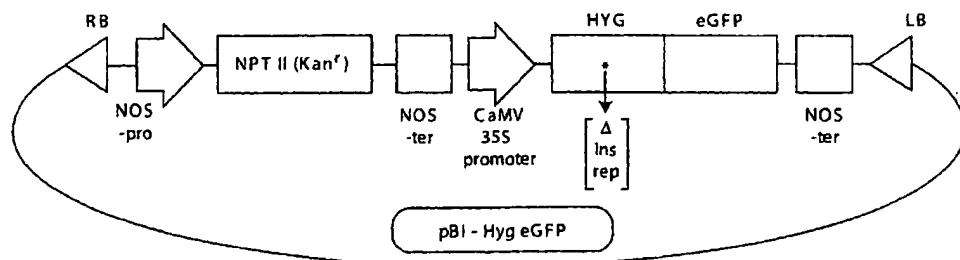
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(54) Title: TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

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(57) Abstract: Presented are methods and compositions for targeted chromosomal genomic alterations with modified single-stranded oligonucleotides. The oligonucleotides of the invention have modified nuclelease-resistant termini comprising LNA, phosphorothioate linkages or 2'-O-Me base analogues or combinations of such modifications.



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**TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS  
USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES**

**Field Of The Invention**

5        The technical field of the invention is oligonucleotide-directed repair or alteration of plant genetic information using novel chemically modified oligonucleotides.

**Background Of The Invention**

A number of methods have been developed specifically to alter the genomic information of plants. These methods generally include the use of vectors such as, for example, T-DNA, carrying nucleic acid sequences encoding partial or complete portions of a particular protein which is expressed in 10 a cell or tissue to effect the alteration. The expression of the particular protein then results in the desired phenotype. See, for example, United States Patent 4,459,355 which describes a method for transforming plants with a DNA vector and United States Patent 5,188,642 which describes cloning or expression vectors containing a transgenic DNA sequence which when expressed in plants confers resistance to the herbicide glyphosate. The use of such transgene-containing vectors adds one or more exogenous copies 15 of a gene in a usually random fashion at one or more integration sites of the plant's genome at some variable frequency. The introduced gene may be foreign or may be derived from the host plant. Any gene which was originally present in the genome, which may be, for example, a normal allelic variant, mutated, defective, and/or functional copy of the introduced gene, is retained in the genome of the host plant.

20        These methods of gene alteration are problematic in that complications which can compromise the vigor, productivity, yield, etc. of the plant may result. One such problem is that insertion of exogenous nucleic acid at random location(s) in the genome can have deleterious effects. The random nature of this insertion and/or the use of exogenous promoters can also cause the timing, location or strength of expression of the introduced transgene to be inappropriate or unpredictable. Another problem 25 with such systems includes the addition of unnecessary and unwanted genetic material to the genome of the recipient, including, for example, T-DNA ends or other vector remnants, exogenous control sequences required to allow production of the transgene protein, which control sequences may be

exogenous or native to the host plant and/or the transgene, and reporter genes or resistance markers. Such remnants and added sequences may have presently unrecognized consequences, for example, involving genetic rearrangements of the recipient genomes. In addition, concerns have been raised with consumption, especially by humans, of plants containing such exogenous genetic material.

5 More recently, simpler systems involving poly- or oligo- nucleotides have been described for use in the alteration of genomic DNA. These chimeric RNA-DNA oligonucleotides, requiring contiguous RNA and DNA bases in a double-stranded molecule folded by complementarity into a double hairpin conformation, have been shown to effect single basepair or frameshift alterations, for example, for mutation or repair of plant, animal or fungal genomes. See, for example, WO 99/07865 and U.S. Patent 10 5,565,350. In the chimeric RNA-DNA oligonucleotide, an uninterrupted stretch of DNA bases within the molecule is required for sequence alteration of the targeted genome while the obligate RNA residues are involved in complex stability. Due to the length, backbone composition, and structural configuration of these chimeric RNA-DNA molecules, they are expensive to synthesize and difficult to purify. Moreover, if the RNA-containing strand of the chimeric RNA-DNA oligonucleotide is designed so as to direct gene 15 alteration, a series of mutagenic reactions resulting in nonspecific base alteration can result. Such a result reduces the utility of such a molecule in methods designed for targeted gene alteration.

Alternatively, other oligo- or poly- nucleotides have been used which require a triplex forming, usually polypurine or polypyrimidine, structural domain which binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide. 20 Such oligonucleotides may have an additional DNA reactive moiety, such as psoralen, covalently linked to the oligonucleotide. These reactive moieties function as effective intercalation agents, stabilize the formation of a triplex and can be mutagenic. Such agents may be required in order to stabilize the triplex forming domain of the oligonucleotide with the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. The utility of 25 these oligonucleotides for directing targeted gene alteration is compromised by a high frequency of nonspecific base changes.

In more recent work, the domain for altering a genome is linked or tethered to the triplex forming domain of the bi-functional oligonucleotide, adding an additional linking or tethering functional domain to the oligonucleotide. See, e.g., Culver et al., Nature Biotechnology 17: 989-93 (1999). Such 30 chimeric or triplex forming molecules have distinct structural requirements for each of the different domains of the complete poly- or oligo-nucleotide in order to effect the desired genomic alteration in either episomal or chromosomal targets.

Other genes, e.g. CFTR, have been targeted by homologous recombination using duplex fragments having several hundred basepairs. See, e.g., Kunzelmann et al., Gene Ther. 3:859-867 (1996). Similar efforts to target genes by homologous recombination in plants using large fragments of DNA had some success. See Kempin et al., Nature 389:802-803 (1997). However, the efficiency and 5 reproducibility of the published homologous recombination approach in plants has severely limited the widespread use of this method.

Earlier experiments to mutagenize an antibiotic resistance indicator gene by homologous recombination used an unmodified DNA oligonucleotide rather than larger fragments of DNA, wherein the oligonucleotide had no functional domains other than a region of complementary sequence to the target. 10 See Campbell et al., New Biologist 1: 223-227 (1989). These experiments required large concentrations of the oligonucleotide, exhibited a very low frequency of episomal modification of a targeted exogenous plasmid gene not normally found in the cell and have not been reproduced. However, as shown in examples herein, we have observed that an unmodified DNA oligonucleotide can convert a base at low frequency which is detectable using the assay systems described herein.

15 Oligonucleotides designed for use in the targeted alteration of genetic information are significantly different from oligonucleotides designed for antisense approaches. For example, antisense oligonucleotides are perfectly complementary to and bind an mRNA strand in order to modify expression of a targeted mRNA and are used at high concentration. As a consequence, they are unable to produce a gene conversion event by either mutagenesis or repair of a defect in the chromosomal DNA of a host 20 genome. Furthermore, the backbone chemical composition used in most oligonucleotides designed for use in antisense approaches renders them inactive as substrates for homologous pairing or mismatch repair enzymes and the high concentrations of oligonucleotide required for antisense applications can be toxic with some types of nucleotide modifications. In addition, antisense oligonucleotides must be complementary to the mRNA and therefore, may not be complementary to the other DNA strand or to 25 genomic sequences that span the junction between intron sequence and exon sequence.

Artificial chromosomes can be useful for the screening purposes identified herein. These molecules are man-made linear or circular DNA molecules constructed from essential cis-acting DNA sequence elements that are responsible for the proper replication and partitioning of natural chromosomes (Murray et al., 1983). The essential elements are: (1) Autonomous Replication Sequences 30 (ARS), (2) Centromeres, and (3) Telomeres.

Yeast artificial chromosomes (YACs) allow large segments of genomic DNA to be cloned and modified (Burke et al., Science 236:806; Peterson et al., Trends Genet. 13:61 (1997); Choi, et al., Nat.

Genet., 4:117-223 (1993), Davies, et al., Biotechnology 11:911-914 (1993), Matsuura, et al., Hum. Mol. Genet., 5:451-459 (1996), Peterson et al., Proc. Natl. Acad. Sci., 93:6605-6609 (1996); and Schedl, et al., Cell, 86:71-82 (1996)). Other vectors also have been developed for the cloning of large segments of genomic DNA, including cosmids, and bacteriophage P1 (Sternberg et al., Proc. Natl. Acad. Sci. U.S.A., 87:103-107 (1990)). YACs have certain advantages over these alternative large capacity cloning vectors (Burke et al., Science, 236:806-812 (1987)). The maximum insert size is 35-30 kb for cosmids, and 100 kb for bacteriophage P1, both of which are much smaller than the maximal insert size for a YAC.

An alternative to YACs are cloning systems based on the *E. coli* fertility factor that have been developed to construct large genomic DNA insert libraries. They are bacterial artificial chromosomes (BACs) and P-1 derived artificial chromosomes (PACs) (Mejia et al., Genome Res. 7:179-186 (1997); Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Ioannou et al., Nat. Genet., 6:84-89 (1994); Hosoda et al., Nucleic Acids Res. 18:3863 (1990)). BACs are based on the *E. coli* fertility plasmid (F factor); and PACs are based on the bacteriophage P1. These vectors propagate at a very low copy number (1-2 per cell) enabling genomic inserts up to 300 kb in size to be stably maintained in recombination deficient hosts. The PACs and BACs are circular DNA molecules that are readily isolated from the host genomic background by classical alkaline lysis (Birnboim et al., Nucleic Acids Res. 7:1513-1523 (1979)). In addition, BACs have been developed for transformation of plants with high-molecular weight DNA using the T-DNA system (Hamilton, *Gene* 24:107-116 (1997); Frary & Hamilton, *Transgenic Res.* 10: 121-132 (2001)).

A need exists for simple, inexpensive oligonucleotides capable of producing targeted alteration of genetic material such as those described herein as well as methods to identify optimal oligonucleotides that accurately and efficiently alter target DNA.

### Summary Of The Invention

Novel, modified single-stranded nucleic acid molecules that direct gene alteration in plants are identified and the efficiency of alteration is analyzed both *in vitro* using a cell-free extract assay and *in vivo* using a yeast system and a plant system. The alteration in an oligonucleotide of the invention may comprise an insertion, deletion, substitution, as well as any combination of these. Site specific alteration of DNA is not only useful for studying function of proteins *in vivo*, but it is also useful for creating plants with desired phenotypes, including, for example, environmental stress tolerance, improved nutritional value, herbicide resistance, disease resistance, modified oil production, modified starch production, and altered floral morphology including selective sterility. As described herein,

oligonucleotides of the invention target directed specific gene alterations in genomic double-stranded DNA in cells. The target genomic DNA can be nuclear chromosomal DNA as well as plastid or mitochondrial chromosomal DNA. The target DNA can also be a transgene present in the plant cell, including; for example, a previously introduced T-DNA. For screening purposes, the target plant DNA can 5 also be extrachromosomal DNA present in plant or non-plant cells in various forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), as well as episomal DNA, including episomal DNA from an exogenous source such as a plasmid or recombinant vector. Many of these artificial chromosome constructs containing plant DNA can be obtained from a variety of sources, 10 including, e.g., the Arabidopsis Biological Resource Center (ABRC) at the Ohio State University, and the Rice Genome Research Program at the MAFF DNA bank in Ibaraki, Japan. The target DNA may be transcriptionally silent or active. In a preferred embodiment, the target DNA to be altered is the non-transcribed strand of a genomic DNA duplex. In a more preferred embodiment, the target DNA to be altered is the non-transcribed strand of a transcribed gene of a genomic DNA duplex.

15 The low efficiency of targeted gene alteration obtained using unmodified DNA oligonucleotides is believed to be largely the result of degradation by nucleases present in the reaction mixture or the target cell. Although different modifications are known to have different effects on the nuclease resistance of oligonucleotides or stability of duplexes formed by such oligonucleotides (see, e.g., Koshkin et al., *J. Am. Chem. Soc.*, 120:13252-3), we have found that it is not possible to predict 20 which of any particular known modification would be most useful for any given alteration event, including for the construction of gene alteration oligonucleotides, because of the interaction of different as yet unidentified proteins during the gene alteration event. Herein, a variety of nucleic acid analogs have been developed that increase the nuclease resistance of oligonucleotides that contain them, including, e.g., nucleotides containing phosphorothioate linkages or 2'-O-methyl analogs. We recently discovered that 25 single-stranded DNA oligonucleotides modified to contain 2'-O-methyl RNA nucleotides or phosphorothioate linkages can enable specific alteration of genetic information at a higher level than either unmodified single-stranded DNA or a chimeric RNA/DNA molecule. See, for example, copending applications United States application no. 60/208,538, United States application no. 60/244,989, United States application no. 09/818,875, international application no. PCT/US01/09761 and Gamper et al., 30 Nucleic Acids Research 28: 4332-4339 (2000), the disclosures of which are incorporated herein in their entirety by reference. We also found that additional nucleic acid analogs which increase the nuclease resistance of oligonucleotides that contain them, including, e.g., "locked nucleic acids" or "LNAs", xylo-

LNAs and L-ribo-LNAs; see, for example, Wengel & Nielsen, WO 99/14226; Wengel, WO 00/56748; Wengel, WO 00/66604; and Jakobsen & Koskin, WO 01/25478 also allow specific targeted alteration of genetic information.

The assay allows for determining the optimum length of the oligonucleotide, optimum sequence of the oligonucleotide, optimum position of the mismatched base or bases, optimum chemical modification or modifications, optimum strand targeted for identifying and selecting the most efficient oligonucleotide for a particular gene alteration event by comparing to a control oligonucleotide. Control oligonucleotides may include a chimeric RNA-DNA double hairpin oligonucleotide directing the same gene alteration event, an oligonucleotide that matches its target completely, an oligonucleotide in which all linkages are phosphorothiolated, an oligonucleotide fully substituted with 2'-O-methyl analogs or an RNA oligonucleotide. Such control oligonucleotides either fail to direct a targeted alteration or do so at a lower efficiency as compared to the oligonucleotides of the invention. The assay further allows for determining the optimum position of a gene alteration event within an oligonucleotide, optimum concentration of the selected oligonucleotide for maximum alteration efficiency by systematically testing a range of concentrations, as well as optimization of either the source of cell extract by testing different plants or strains, or testing cells derived from different plants or strains, or plant cell lines. Using a series of single-stranded oligonucleotides, comprising all RNA or DNA residues and various mixtures of the two, several new structures are identified as viable molecules in nucleotide conversion to direct or repair a genomic mutagenic event. When extracts from mammalian, plant and fungal cells are used and are analyzed using a genetic readout assay in bacteria, single-stranded oligonucleotides having one of several modifications are found to be more active than a control RNA-DNA double hairpin chimera structure when evaluated using an *in vitro* gene repair assay. Similar results are also observed *in vivo* using yeast, mammalian and plant cells. Molecules containing various lengths of modified bases were found to possess greater activity than unmodified single-stranded DNA molecules.

25 **Detailed Description Of The Invention**

The present invention provides oligonucleotides having chemically modified, nuclease resistant residues, preferably at or near the termini of the oligonucleotides, and methods for their identification and use in targeted alteration of plant genetic material, including gene mutation, targeted gene repair and gene knockout. The oligonucleotides are preferably used for mismatch repair or alteration by changing at least one nucleic acid base, or for frameshift repair or alteration by addition or deletion of at least one nucleic acid base. The oligonucleotides of the invention direct any such alteration,

including gene correction, gene repair or gene mutation and can be used, for example, to introduce a polymorphism or haplotype or to eliminate ("knockout") a particular protein activity. For example, gene alterations that knockout a particular protein activity can be obtained using oligonucleotides designed to convert a codon in the coding region of the protein to a stop codon, thus prematurely terminating

5 translation of the protein. Oligonucleotides that introduce stop codons in the open-reading-frame of the protein are one embodiment of the invention. Generally, oligonucleotides that introduce stop codons early in the open-reading-frame of the protein are preferred. If the open-reading-frame contains more than one methionine, oligonucleotides that introduce stop codons after the second methionine are preferred. Additionally, if the gene exhibits alternative splice sites, oligonucleotides that introduce stop

10 codons in exons after the alternative splice site are preferred. The following table provides examples of codons that can be converted to stop codons by altering a single oligonucleotide. A skilled artisan could readily identify other codons that can be converted to stop codons by altering one, two or three of the base pairs in a given codon. Similarly, a skilled artisan could readily identify codons that can be converted to stop codons by a frameshift mutation that inserts or deletes one or two base pairs in the

15 open-reading-frame. It is also understood that more than one stop codon can be generated in a single open-reading-frame and that these stop codons can be adjacent in the sequence or separated by intervening codons. Where more than one stop codon is introduced into a single open-reading-frame, such alterations can be generated by a single or multiple oligonucleotides and can be generated simultaneously or by sequential mutagenesis of the target nucleic acid.

20	Original codons*	Corresponding stop codon
	<u>G</u> GA (glycine), <u>A</u> GA (arginine), <u>C</u> GA (arginine), <u>T</u> <u>T</u> A (leucine), <u>T</u> <u>C</u> A (serine), <u>T</u> <u>G</u> T (cysteine), <u>T</u> <u>G</u> <u>G</u> (tryptophan), <u>T</u> <u>G</u> <u>C</u> (cysteine)	TGA
	<u>A</u> AG (lysine), <u>G</u> AG (glutamate), <u>C</u> AG (glutamine), <u>T</u> <u>T</u> G (leucine), <u>T</u> <u>C</u> G (serine), <u>T</u> <u>G</u> <u>G</u> (tryptophan), <u>T</u> <u>A</u> T (cysteine), <u>T</u> <u>A</u> <u>C</u> (tyrosine)	TAG
25	<u>A</u> AA (lysine), <u>G</u> AA (glutamate), <u>C</u> AA (glutamine), <u>T</u> <u>T</u> A (leucine), <u>T</u> <u>C</u> A (serine), <u>T</u> <u>A</u> T (cysteine), <u>T</u> <u>A</u> <u>C</u> (tyrosine)	TAA

\*The amino acid encoded by the original codon is shown in parentheses and the base targeted for alteration to convert the codon to the corresponding stop codon is underlined and in bold

The oligonucleotides of the invention are designed as substrates for homologous pairing and repair enzymes and as such have a unique backbone composition that differs from chimeric RNA-DNA double hairpin oligonucleotides, antisense oligonucleotides, and/or other poly- or oligo-nucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligo-  
5 nucleotides described herein are inexpensive to synthesize and easy to purify. In side-by-side comparisons, an optimized single-stranded oligonucleotide comprising modified residues as described herein is significantly more efficient than a chimeric RNA-DNA double hairpin oligonucleotide in directing a base substitution or frameshift mutation in a cell-free extract assay.

We have discovered that single-stranded oligonucleotides having a DNA domain  
10 surrounding the targeted base, with the domain preferably central to the poly- or oligo-nucleotide, and having at least one modified end, preferably at the 3' terminal region, are able to alter a target genetic sequence and with an efficiency that is higher than chimeric RNA-DNA double hairpin oligonucleotides disclosed in US Patent 5,565,350. Preferred oligonucleotides of the invention have at least two modified bases on at least one of the termini, preferably the 3' terminus of the oligonucleotide. Oligonucleotides  
15 of the invention can efficiently be used to introduce targeted alterations in a genetic sequence of DNA in the presence of human, animal, plant, fungal (including yeast) proteins and in cells of different types including, for example, plant cells, fungal cells including *S. cerevisiae*, *Ustilago maydis*, *Candida albicans*, and mammalian cells. Particularly preferred are cells and cell extracts derived from plants including, for example, experimental model plants such as *Chlamydomonas reinhardtii*, *Physcomitrella patens*, and  
20 *Arabidopsis thaliana* in addition to crop plants such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apples (*Malus*, e.g. *domesticus*), mangoes (*Mangifera*, e.g. *indica*), banana (*Musa*, e.g. *acuminata*), berries (such as currant, *Ribes*, e.g. *rubrum*), kiwifruit (*Actinidia*, e.g. *chinensis*), grapes (*Vitis*, e.g. *vinifera*), bell peppers (*Capsicum*, e.g. *annuum*), cherries (such as the sweet cherry, *Prunus*, e.g. *avium*), cucumber (*Cucumis*, e.g. *sativus*), melons (*Cucumis*, e.g. *melo*), nuts (such as  
25 walnut, *Juglans*, e.g. *regia*; peanut, *Arachis hypogaea*), orange (*Citrus*, e.g. *maxima*), peach (*Prunus*, e.g. *persica*), pear (*Pyrus*, e.g. *communis*), plum (*Prunus*, e.g. *domestica*), strawberry (*Fragaria*, e.g. *moschata* or *vesca*), tomato (*Lycopersicon*, e.g. *esculentum*); leaves and forage, such as alfalfa (*Medicago*, e.g. *sativa* or *truncatula*), cabbage (e.g. *Brassica oleracea*), endive (*Cichoreum*, e.g. *endivia*), leek (*Allium*, e.g. *porrum*), lettuce (*Lactuca*, e.g. *sativa*), spinach (*Spinacia*, e.g. *oleracea*), tobacco (*Nicotiana*, e.g. *tabacum*); roots, such as arrowroot (*Maranta*, e.g. *arundinacea*), beet (*Beta*, e.g. *vulgaris*), carrot  
30 (*Daucus*, e.g. *carota*), cassava (*Manihot*, e.g. *esculenta*), turnip (*Brassica*, e.g. *rapa*), radish (*Raphanus*, e.g. *sativus*), yam (*Dioscorea*, e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, including oilseeds,

such as beans (*Phaseolus*, e.g. *vulgaris*), pea (*Pisum*, e.g. *sativum*), soybean (*Glycine*, e.g. *max*), cowpea (*Vigna unguiculata*), mothbean (*Vigna aconitifolia*), wheat (*Triticum*, e.g. *aestivum*), sorghum (*Sorghum* e.g. *bicolor*), barley (*Hordeum*, e.g. *vulgare*), corn (*Zea*, e.g. *mays*), rice (*Oryza*, e.g. *sativa*), rapeseed (*Brassica napus*), millet (*Panicum* sp.), sunflower (*Helianthus annuus*), oats (*Avena sativa*),  
5. chickpea (*Cicer*, e.g. *arietinum*); tubers, such as kohlrabi (*Brassica*, e.g. *oleraceae*), potato (*Solanum*, e.g. *tuberosum*) and the like; fiber and wood plants, such as flax (*Linum* e.g. *usitatissimum*), cotton (*Gossypium* e.g. *hirsutum*), pine (*Pinus* sp.), oak (*Quercus* sp.), eucalyptus (*Eucalyptus* sp.), and the like and ornamental plants such as turfgrass (*Lolium*, e.g. *rigidum*), petunia (*Petunia*, e.g. *x hybrida*), hyacinth (*Hyacinthus orientalis*), carnation (*Dianthus* e.g. *caryophyllus*), delphinium (*Delphinium*, e.g. *ajacis*), Job's tears (*Coix lacryma-jobi*), snapdragon (*Antirrhinum majus*), poppy (*Papaver*, e.g. *nudicaule*), lilac (*Syringa*, e.g. *vulgaris*), hydrangea (*Hydrangea* e.g. *macrophylla*), roses (including Gallicas, Albas, Damasks, Damask Perpetuals, Centifolias, Chinas, Teas and Hybrid Teas) and ornamental goldenrods (e.g. *Solidago* spp.). Such plant cells can then be used to regenerate whole plants according to methods described herein or any method known in the art. The DNA domain of the oligonucleotides is preferably  
10 fully complementary to one strand of the gene target, except for the mismatch base or bases responsible for the gene alteration event(s). On either side of the preferably central DNA domain, the contiguous bases may be either RNA bases or, preferably, are primarily DNA bases. The central DNA domain is generally at least 8 nucleotides in length. The base(s) targeted for alteration in the most preferred  
15 embodiments are at least about 8, 9 or 10 bases from one end of the oligonucleotide.

According to certain embodiments, one or both of the termini of the oligonucleotides of the present invention comprise phosphorothioate modifications, LNA backbone (including LNA derivatives and analogs) modifications, or 2'-O-methyl base analogs, or any combination of these modifications. Oligonucleotides comprising 2'-O-methyl or LNA analogs are a mixed DNA/RNA polymer. The oligonucleotides of the invention are, however, single-stranded and are not designed to form a stable internal duplex structure within the oligonucleotide. The efficiency of gene alteration is surprisingly increased with oligonucleotides having internal complementary sequence comprising phosphorothioate modified bases as compared to 2'-O-methyl modifications. This result indicates that specific chemical interactions are involved between the converting oligonucleotide and the proteins involved in the conversion. The effect of other such chemical interactions to produce nuclease resistant termini using modifications other than LNA (including LNA derivatives or analogs), phosphorothioate linkages, or 2'-O-methyl analog incorporation into an oligonucleotide can not yet be predicted because the proteins  
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involved in the alteration process and their particular chemical interaction with the oligonucleotide substituents are not yet known and cannot be predicted.

In the examples, oligonucleotides of defined sequence are provided for alteration of genes in particular plants. Provided the teachings of the instant application, one of skill in the art could readily design oligonucleotides to introduce analogous alterations in homologous genes from any plant. Furthermore, in the tables of these examples, the oligonucleotides of the invention are not limited to the particular sequences disclosed. The oligonucleotides of the invention include extensions of the appropriate sequence of the longer 120 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Thus the oligonucleotides of the invention include for each correcting change, oligonucleotides of length 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. In some embodiments, longer nucleic acids of up to 240 bases which comprise the sequences disclosed herein may be used. Moreover, the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides of the invention as disclosed in the various tables for alteration of particular plant genes contain phosphorothioate linkages, 2'-O-methyl analog or LNA (including LNA derivatives and analogs) or any combination of these modifications just as the assay oligonucleotides do.

The present invention, however, is not limited to oligonucleotides that contain any particular nuclease resistant modification. Oligonucleotides of the invention may be altered with any combination of additional LNAs (including LNA derivatives and analogs), phosphorothioate linkages or 2'-O-methyl analogs to maximize conversion efficiency. For oligonucleotides of the invention that are longer than about 17 to about 25 bases in length, internal as well as terminal region segments of the backbone may be altered. Alternatively, simple fold-back structures at each end of a oligonucleotide or appended end groups may be used in addition to a modified backbone for conferring additional nuclease resistance.

The different oligonucleotides of the present invention preferably contain more than one of the aforementioned backbone modifications at each end. In some embodiments, the backbone modifications are adjacent to one another. However, the optimal number and placement of backbone modifications for any individual oligonucleotide will vary with the length of the oligonucleotide and the particular type of backbone modification(s) that are used. If constructs of identical sequence having

phosphorothioate linkages are compared, 2, 3, 4, 5, or 6 phosphorothioate linkages at each end are preferred. If constructs of identical sequence having 2'-O-methyl base analogs are compared, 1, 2, 3 or 4 analogs are preferred. The optimal number and type of backbone modifications for any particular oligonucleotide useful for altering target DNA may be determined empirically by comparing the alteration 5 efficiency of the oligonucleotide comprising any combination of the modifications to a control molecule of comparable sequence using any of the assays described herein. The optimal position(s) for oligonucleotide modifications for a maximally efficient altering oligonucleotide can be determined by testing the various modifications as compared to control molecule of comparable sequence in one of the assays disclosed herein. In such assays, a control molecule includes, e.g., a completely 2'-O-methyl 10 substituted molecule, a completely complementary oligonucleotide, or a chimeric RNA-DNA double hairpin.

Increasing the number of phosphorothioate linkages, LNAs or 2'-O-methyl bases beyond the preferred number generally decreases the gene repair activity of a 25 nucleotide long oligonucleotide. Based on analysis of the concentration of oligonucleotide present in the extract after different time periods 15 of incubation, it is believed that the terminal modifications impart nuclease resistance to the oligonucleotide thereby allowing it to survive within the cellular environment. However, this may not be the only possible mechanism by which such modifications confer greater efficiency of conversion. For example, as disclosed herein, certain modifications to oligonucleotides confer a greater improvement to the efficiency of conversion than other modifications.

Efficiency of conversion is defined herein as the percentage of recovered substrate 20 molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. the genome of a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be sequenced to determine the percentage that have acquired 25 the desire change. The oligonucleotides of the invention in different embodiments can alter DNA two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold more than control oligonucleotides. Such control oligonucleotides are oligonucleotides with fully phosphorothiolated linkages, oligonucleotides that are fully substituted with 2'-O-methyl analogs, a perfectly matched oligonucleotide that is fully complementary to a target sequence or a chimeric DNA-RNA double hairpin 30 oligonucleotide such as disclosed in US Patent 5,565,350.

In addition, for a given oligonucleotide length, additional modifications interfere with the ability of the oligonucleotide to act in concert with the cellular recombination or repair enzyme machinery

which is necessary and required to mediate a targeted substitution, addition or deletion event in DNA. For example, fully phosphorothiolated or fully 2-O-methylated molecules are inefficient in targeted gene alteration.

The oligonucleotides of the invention as optimized for the purpose of targeted alteration of genetic material, including gene knockout or repair, are different in structure from antisense oligonucleotides that may possess a similar mixed chemical composition backbone. The oligonucleotides of the invention differ from such antisense oligonucleotides in chemical composition, structure, sequence, and in their ability to alter genomic DNA. Significantly, antisense oligonucleotides fail to direct targeted gene alteration. The oligonucleotides of the invention may target either strand of DNA and can include any component of the genome including, for example, intron and exon sequences. The preferred embodiment of the invention is a modified oligonucleotide that binds to the non-transcribed strand of a genomic DNA duplex. In other words, the preferred oligonucleotides of the invention target the sense strand of the DNA, i.e. the oligonucleotides of the invention are complementary to the non-transcribed strand of the target duplex DNA. The sequence of the non-transcribed strand of a DNA duplex is found in the mRNA produced from that duplex, given that mRNA uses uracil-containing nucleotides in place of thymine-containing nucleotides.

Moreover, the initial observation that single-stranded oligonucleotides comprising these modifications and lacking any particular triplex forming domain have reproducibly enhanced gene alteration activity in a variety of assay systems as compared to a chimeric RNA-DNA double-stranded hairpin control or single-stranded oligonucleotides comprising other backbone modifications was surprising. The single-stranded molecules of the invention totally lack the complementary RNA binding structure that stabilizes a normal chimeric double-stranded hairpin of the type disclosed in U.S. Patent 5,565,350 yet is more effective in producing targeted base conversion as compared to such a chimeric RNA-DNA double-stranded hairpin. In addition, the molecules of the invention lack any particular triplex forming domain involved in Hoogsteen interactions with the DNA double helix and required by other known oligonucleotides in other oligonucleotide-dependant gene conversion systems. Although the lack of these functional domains was expected to decrease the efficiency of an alteration in a sequence, just the opposite occurs: the efficiency of sequence alteration using the modified oligonucleotides of the invention is higher than the efficiency of sequence alteration using a chimeric RNA-DNA hairpin targeting the same sequence alteration. Moreover, the efficiency of sequence alteration or gene conversion directed by an unmodified oligonucleotide is many times lower as compared to a control chimeric RNA-DNA molecule or the modified oligonucleotides of the invention targeting the

same sequence alteration. Similarly, molecules containing at least 3 2'-O-methyl base analogs are about four to five fold less efficient as compared to an oligonucleotide having the same number of phosphorothioate linkages.

The oligonucleotides of the present invention for alteration of a single base are about 17 to about 121 nucleotides in length, preferably about 17 to about 74 nucleotides in length. Most preferably, however, the oligonucleotides of the present invention are at least about 25 bases in length, unless there are self-dimerization structures within the oligonucleotide. If the oligonucleotide has such an unfavorable structure, lengths longer than 35 bases are preferred. Oligonucleotides with modified ends both shorter and longer than certain of the exemplified, modified oligonucleotides herein function as gene repair or gene knockout agents and are within the scope of the present invention.

Once an oligomer is chosen, it can be tested for its tendency to self-dimerize, since self-dimerization may result in reduced efficiency of alteration of genetic information. Checking for self-dimerization tendency can be accomplished manually or, preferably, using a software program. One such program is Oligo Analyzer 2.0, available through Integrated DNA Technologies (Coralville, IA 52241) (<http://www.idtdna.com>); this program is available for use on the world wide web at

<http://www.idtdna.com/program/oligoanalyzer/>

oligoanalyzer.asp.

For each oligonucleotide sequence input into the program, Oligo Analyzer 2.0 reports possible self-dimerized duplex forms, which are usually only partially duplexed, along with the free energy change associated with such self-dimerization. Delta G-values that are negative and large in magnitude, indicating strong self-dimerization potential, are automatically flagged by the software as "bad". Another software program that analyzes oligomers for pair dimer formation is Primer Select from DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715, Phone: (608) 258-7420 (<http://www.dnastar.com/products/PrimerSelect.html>).

If the sequence is subject to significant self-dimerization, the addition of further sequence flanking the "repair" nucleotide can improve gene correction frequency.

Generally, the oligonucleotides of the present invention are identical in sequence to one strand of the target DNA, which can be either strand of the target DNA, with the exception of one or more targeted bases positioned within the DNA domain of the oligonucleotide, and preferably toward the middle between the modified terminal regions. Preferably, the difference in sequence of the oligonucleotide as compared to the targeted genomic DNA is located at about the middle of the oligonucleotide sequence. In a preferred embodiment, the oligonucleotides of the invention are complementary to the non-transcribed

strand of a duplex. In other words, the preferred oligonucleotides target the sense strand of the DNA, i.e. the oligonucleotides of the invention are preferably complementary to the strand of the target DNA the sequence of which is found in the mRNA.

The oligonucleotides of the invention can include more than a single base change. In an 5 oligonucleotide that is about a 70-mer, with at least one modified residue incorporated on the ends, as disclosed herein, multiple bases can be simultaneously targeted for change. The target bases may be up to 27 nucleotides apart and may not be changed together in all resultant plasmids in all cases. There is a frequency distribution such that the closer the target bases are to each other in the central DNA domain, within the oligonucleotides of the invention, the higher the frequency of change in a given cell. Target 10 bases only two nucleotides apart are changed together in every case that has been analyzed. The farther apart the two target bases are, the less frequent the simultaneous change. Thus, oligonucleotides of the invention may be used to repair or alter multiple bases rather than just one single base. For example, in a 74-mer oligonucleotide having a central base targeted for change, a base change event up to about 27 nucleotides away can also be effected. The positions of the altering bases within the 15 oligonucleotide can be optimized using any one of the assays described herein. Preferably, the altering bases are at least about 8 nucleotides from one end of the oligonucleotide.

The oligonucleotides of the present invention can be introduced into cells by any suitable means. According to certain preferred embodiments, the modified oligonucleotides may be used alone. Suitable means, however, include the use of polycations, cationic lipids, liposomes, polyethylenimine 20 (PEI), electroporation, biolistics, microinjection and other methods known in the art to facilitate cellular uptake. For plant cells, biolistic or particle bombardment methods are typically used. According to certain preferred embodiments of the present invention, isolated plant cells are treated in culture according to the methods of the invention, to mutate or repair a target gene. Alternatively, plant target DNA may be modified *in vitro* or in another cell type, including for example, yeast or bacterial cells and then introduced 25 into a plant cell as, for example, a T-DNA. Plant cells thus modified may be used to regenerate the whole organism as, for example, in a plant having a desired targeted genomic change. In other instances, targeted genomic alteration, including repair or mutagenesis, may take place *in vivo* following direct administration of the modified, single-stranded oligonucleotides of the invention to a subject.

The single-stranded, modified oligonucleotides of the present invention have numerous 30 applications as gene repair, gene modification, or gene knockout agents. Such oligonucleotides may be advantageously used, for example, to introduce or correct multiple point mutations. Each mutation leads to the addition, deletion or substitution of at least one base pair. The methods of the present invention

offer distinct advantages over other methods of altering the genetic makeup of an organism, in that only the individually targeted bases are altered. No additional foreign DNA sequences are added to the genetic complement of the organism. Such agents may, for example, be used to develop plants with improved traits by rationally changing the sequence of selected genes in isolated cells and using these 5 modified cells to regenerate whole plants having the altered gene. See, e.g., U.S. Patent 6,046,380 and U.S. Patent 5,905,185 incorporated herein by reference. Such plants produced using the compositions of the invention lack additional undesirable selectable markers or other foreign DNA sequences. Targeted base pair substitution or frameshift mutations introduced by an oligonucleotide in the presence of a cell-free extract also provides a way to modify the sequence of extrachromosomal elements, including, for 10 example, plasmids, cosmids and artificial chromosomes. The oligonucleotides of the invention also simplify the production of plants having particular modified or inactivated genes. Altered plant model systems such as those produced using the methods and oligonucleotides of the invention are invaluable in determining the function of a gene and in evaluating drugs. The oligonucleotides and methods of the present invention may also be used to introduce molecular markers, including, for example, SNPs, 15 RFLPs, AFLPs and CAPs.

The purified oligonucleotide compositions may be formulated in accordance with routine procedures depending on the target. For example, purified oligonucleotide can be used directly in a standard reaction mixture to introduce alterations into targeted DNA *in vitro* or where cells are the target as a composition adapted for bathing cells in culture or for microinjection into cells in culture. The purified 20 oligonucleotide compositions may also be provided on coated microbeads for biolistic delivery into plant cells. Where necessary, the composition may also include a solubilizing agent. Generally, the ingredients will be supplied either separately or mixed together in single-use form, for example, as a dry, lyophilized powder or water-free concentrate. In general, dosage required for efficient targeted gene alteration will range from about 0.001 to 50,000  $\mu$ g/kg target tissue, preferably between 1 to 250  $\mu$ g/kg, 25 and most preferably at a concentration of between 30 and 60 micromolar.

For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In a preferred method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim) or an equivalent 30 such as lipofectin. The amount of the oligonucleotide used is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells. For electroporation, between 20 and 2000 nanograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve

efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein. For biolistic delivery, microbeads are generally coated with resuspended oligonucleotides, which range of oligonucleotide to microbead concentration can be similarly adjusted to improve efficiency as determined using one of the assay methods described herein, starting with about 5 0.05 to 1 microgram of oligonucleotide to 25 microgram of 1.0 micrometer gold beads or similar microcarrier.

Another aspect of the invention is a kit comprising at least one oligonucleotide of the invention. The kit may comprise an additional reagent or article of manufacture. The additional reagent or article of manufacture may comprise a delivery mechanism, cell extract, a cell, or a plasmid, such as 10 one of those disclosed in the Figures herein, for use in an assay of the invention. Alternatively, the invention includes a kit comprising an isogenic set of cells in which each cell in the kit comprises a different altered amino acid for a target protein encoded by a targeted altered gene within the cell produced according to the methods of the invention.

#### Brief Description Of The Drawings

15 Figure 1. *Flow diagram for the generation of modified single-stranded oligonucleotides.* The upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (A) 2'-O-methyl RNA nucleotides or (B) phosphorothioate linkages. Fold changes in repair activity for correction of kan<sup>s</sup> in the HUH7 cell-free extract are presented in parenthesis. HUH7 cells are described in Nakabayashi et al., Cancer Research 42: 3858-3863 (1982). Each single-stranded oligonucleotide is 25 bases in length and contains a G 20 residue mismatched to the complementary sequence of the kan<sup>s</sup> gene. The numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the molecule. Hence oligo 12S/25G contains an all phosphorothioate backbone, displayed as a dotted line. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA 25 residues and the carat indicates the mismatched base site (G). Figure 1(C) provides a schematic plasmid indicating the sequence of the kan chimeric double-stranded hairpin oligonucleotide (left) and the sequence the tet chimeric double-stranded hairpin oligonucleotide used in other experiments. Figure 1(D) provides a flow chart of a kan experiment in which a chimeric double-stranded hairpin oligonucleotide is used.

30 Figure 2. *Genetic readout system for correction of a point mutation in plasmid pK<sup>s</sup>m4021.* A mutant kanamycin gene harbored in plasmid pK<sup>s</sup>m4021 is the target for correction by oligonucleotides.

The mutant G is converted to a C by the action of the oligo. Corrected plasmids confer resistance to kanamycin in *E.coli* (DH10B) after electroporation leading to the genetic readout and colony counts.

Figure 3: *Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides.* (A) Plasmid pT<sup>s</sup>Δ208 contains a single base deletion mutation at position 208 rendering it unable to confer tet resistance. The target sequence presented below indicates the insertion of a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) DNA sequence confirming base insertion directed by Tet 3S/25G; the yellow highlight indicates the position of frameshift repair.

Figure 4. *DNA sequences of representative kan' colonies.* Confirmation of sequence alteration directed by the indicated molecule is presented along with a table outlining codon distribution. Note that 10S/25G and 12S/25G elicit both mixed and unfaithful gene repair. The number of clones sequenced is listed in parentheses next to the designation for the single-stranded oligonucleotide. A plus (+) symbol indicates the codon identified while a figure after the (+) symbol indicates the number of colonies with a particular sequence. TAC/TAG indicates a mixed peak. Representative DNA sequences are presented below the table with yellow highlighting altered residues.

Figure 5. *Gene correction in HeLa cells.* Representative oligonucleotides of the invention are co-transfected with the pCMVneo(')FIAsH plasmid (shown in Figure 9) into HeLa cells. Ligand is diffused into cells after co-transfection of plasmid and oligonucleotides. Green fluorescence indicates gene correction of the mutation in the antibiotic resistance gene. Correction of the mutation results in the expression of a fusion protein that carries a marker ligand binding site and when the fusion protein binds the ligand, a green fluorescence is emitted. The ligand is produced by Aurora Biosciences and can readily diffuse into cells enabling a measurement of corrected protein function; the protein must bind the ligand directly to induce fluorescence. Hence cells bearing the corrected plasmid gene appear green while "uncorrected" cells remain colorless.

Figure 6. *Z-series imaging of corrected cells.* Serial cross-sections of the HeLa cell represented in Figure 5 are produced by Zeiss 510 LSM confocal microscope revealing that the fusion protein is contained within the cell.

Figure 7. *Hygromycin-eGFP target plasmids.* (A) Plasmid pAURHYG(ins)GFP contains a single base insertion mutation between nucleotides 136 and 137, at codon 46, of the Hygromycin B coding sequence (cds) which is transcribed from the constitutive ADH1 promoter. The target sequence presented below indicates the deletion of an A and the substitution of a C for a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) Plasmid pAURHYG(rep)GFP contains a

base substitution mutation introducing a G at nucleotide 137, at codon 46, of the Hygromycin B coding sequence (cds). The target sequence presented below the diagram indicates the amino acid conservative replacement of G with C, restoring gene function.

5 Figure 8. *Oligonucleotides for correction of hygromycin resistance gene.* The sequence of the oligonucleotides used in experiments to assay correction of a hygromycin resistance gene are shown. DNA residues are shown in capital letters, RNA residues are shown in lowercase and nucleotides with a phosphorothioate backbone are capitalized and underlined.

Figure 9. *pAURNeo(-)FIAsh plasmid.* This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence.

10 Figure 10. *pYESHyg(x)eGFP plasmid.* This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in Figure 7, except the promoter is the inducible GAL1 promoter. This promoter is inducible with galactose, leaky in the presence of raffinose, and repressed in the presence of dextrose.

15 Figure 11. *pBI-HygeGFP plasmid.* This plasmid is a construct based on the plasmids pBI101, pBI 101.2, pBI101.3 or pBI 121 available from Clontech in which HygeGFP replaces the beta-glucuronidase gene of the Clontech plasmids. The different Clontech plasmids vary by a reading frame shift relative to the polylinker, or the presence of the Cauliflower mosaic virus promoter.

The following examples are provided by way of illustration only, and are not intended to limit the scope of the invention disclosed herein.

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#### EXAMPLE 1 Assay Method For Base Alteration And Preferred Oligonucleotide Selection

In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see Figure 1 for structures (A and B) and sequences (C and D) of assay oligonucleotides) are used to correct a point mutation in the kanamycin gene of pK<sup>s</sup>m4021 (Figure 2) or the tetracycline gene of pT<sup>s</sup>Δ208 (Figure 3). All kan oligonucleotides share the same 25 base sequence surrounding the target base identified for change, just as all tet oligonucleotides do. The sequence is given in Figures 1C and Figure 1D. Each plasmid contains a functional ampicillin gene. Kanamycin gene function is restored when a G at position 4021 is converted to a C (via a substitution mutation); tetracycline gene function is restored when a deletion at position 208 is replaced by a C (via frameshift mutation). A separate plasmid, pAURNeo(-)FIAsh (Figure 9), bearing the kan<sup>s</sup> gene is used in the cell culture experiments. This plasmid was constructed by inserting a synthetic expression cassette containing a neomycin phosphotransferase

(kanamycin resistance) gene and an extended reading frame that encodes a receptor for the FlAsH ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, WI). The resulting construct replicates in *S. cerevisiae* at low copy number, confers resistance to aureobasidinA and constitutively expresses either the Neo+/FlAsH fusion product (after alteration) or the truncated Neo-/FlAsH product (before alteration) from the ADH1 promoter. By extending the reading frame of this gene to code for a unique peptide sequence capable of binding a small ligand to form a fluorescent complex, restoration of expression by correction of the stop codon can be detected in real time using confocal microscopy.

Additional constructs can be made to test additional gene alteration events or for specific use in different expression systems. For example, alternative comparable plant plasmids or integration vectors such as, e.g. those based on T-DNA, can be constructed for stable expression in plant cells according to the disclosures herein. Such constructs would use a plant specific promoter such as, e.g., cauliflower mosaic virus 35S promoter, to replace the promoters directing expression of the neo, hyg or aureobasidinA resistance gene disclosed herein, including for example, in Figures 7B, 9 and 10 herein. Moreover, the green fluorescent protein (GFP) sequence used herein may be modified to increase expression in plant cells such as Arabidopsis and the other plants disclosed herein as described in Haseloff et al., Proc. Natl. Acad. Sci. 94(6): 2122-7 (1997), Rouwendal et al. Plant Mol. Biol. 33(6): 989-99 (1997) and Hu et al. FEBS Lett. 369(2-3): 331-4 (1995). Codon usage for optimal expression of GFP in plants results from increasing the frequency of codons with a C or a G in the third position from 32 to about 60%. Specific constructs are disclosed and can be used as follows with such plant specific alterations.

We also construct three mammalian expression vectors, pHyg(rep)eGFP, pHyg(Δ)eGFP, pHyg(ins)eGFP, that contain a substitution mutation at nucleotide 137 of the hygromycin-B coding sequence. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. All point mutations create a nonsense termination codon at residue 46. We use pHYGeGFP plasmid (Invitrogen, CA) DNA as a template to introduce the mutations into the hygromycin-eGFP fusion gene by a two step site-directed mutagenesis PCR protocol. First, we generate overlapping 5' and a 3' amplicons surrounding the mutation site by PCR for each of the point mutation sites. A 215 bp 5' amplicon for the (rep), (Δ) or (ins) was generated by polymerization from oligonucleotide primer HygEGFPf (5'-AATACGACTCACTATAGG-3') to primer Hygrepr (5'GACCTATCCACGCCCTCC-3'), HygΔr (5'-GACTATCCACGCCCTCC-3'), or Hyginsr (5'-GACATTATCCACGCCCTCC-3'), respectively. We generate a 300bp 3' amplicon for the (rep), (Δ) or (ins) by polymerization from oligonucleotide primers Hygrefp (5'-CTGGGATAGGTCTGCGG-3'), HygΔf

(5'-CGTGGATAGTCCTGCGG-3'), Hyginsf (5'-CGTGGATAATGTCCCTGCGG-3'), respectively to primer HygEGFPr (5'-AAATCACGCCATGTAGTG-3'). We mix 20 ng of each of the resultant 5' and 3' overlapping amplicon mutation sets and use the mixture as a template to amplify a 523 bp fragment of the Hygromycin gene spanning the KpnI and RsrII restriction endonuclease sites. We use the Expand PCR system (Roche) to generate all amplicons with 25 cycles of denaturing at 94°C for 10 seconds, annealing at 55°C for 20 seconds and elongation at 68°C for 1 minute. We digest 10 µg of vector pHYGeGFP and 5 µg of the resulting fragments for each mutation with KpnI and RsrII (NEB) and gel purify the fragment for enzymatic ligation. We ligate each mutated insert into pHYGeGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm the mutation by Sanger dideoxy chain termination sequencing and purify the plasmid using a Qiagen maxiprep kit.

10 *Oligonucleotide synthesis and cells.* Chimeric oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) are synthesized using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, each oligonucleotide is gel-purified using, for example, procedures such as those described in 15 Gamper *et al.*, *Biochem.* 39, 5808-5816 (2000) and the concentrations determined spectrophotometrically (33 or 40 µg/ml per A<sub>260</sub> unit of single-stranded or hairpin oligomer). HUH7 cells are grown in DMEM, 10% FBS, 2mM glutamine, 0.5% pen/strep. The *E.coli* strain, DH10B, is obtained from Life Technologies (Gaithersburg, MD); DH10B cells contain a mutation in the RECA gene (*recA*).

20 *Cell-free extracts.* Although this portion of this example is directed to mammalian systems, similar extracts from plants can be prepared as disclosed elsewhere in this application and used as disclosed in this example. We prepare cell-free extracts from HUH7 cells or other mammalian cells, as follows. We employ this protocol with essentially any mammalian cell including, for example, H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C127I (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma). We harvest approximately 2x10<sup>8</sup> cells. We then wash the cells immediately in cold hypotonic buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM MgCl<sub>2</sub>; 1 mM DTT) with 250 mM sucrose. We then resuspend the cells in cold hypotonic buffer without sucrose and after 15 minutes we lyse the cells with 25 strokes of a Dounce homogenizer using a tight fitting pestle. We incubate the lysed cells for 25 60 minutes on ice and centrifuge the sample for 15 minutes at 12000xg. The cytoplasmic fraction is 30 enriched with nuclear proteins due to the extended co-incubation of the fractions following cell breakage.

We then immediately aliquote and freeze the supernatant at -80°C. We determine the protein concentration in the extract by the Bradford assay.

We also perform these experiments with cell-free extracts obtained from fungal cells, including, for example, *S. cerevisiae* (yeast), *Ustilago maydis*, and *Candida albicans*. For example, we grow yeast cells into log phase in 2L YPD medium for 3 days at 30°C. We then centrifuge the cultures at 5000xg, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1mM EDTA lysis solution and freeze them on dry ice. After thawing, we add KCl, spermidine and lyticase to final concentrations of 0.25 mM, 5 mM and 0.1 mg/ml, respectively. We incubate the suspension on ice for 60 minutes, add PMSF and Triton X100 to final concentrations of 0.1 mM and 0.1% and continue to incubate on ice for 20 minutes. We centrifuge the lysate at 3000xg for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000xg for 15 minutes. We then add glycerol to the clarified extract to a concentration of 10% (v/v) and freeze aliquots at -80°C. We determine the protein concentration of the extract by the Bradford assay.

Reaction mixtures of 50 µl are used, consisting of 10-30 µg protein of cell-free extract, which can be optionally substituted with purified proteins or enriched fractions, about 1.5 µg chimeric double-hairpin oligonucleotide or 0.55 µg single-stranded molecule (3S/25G or 6S/25G, see Figure 1), and 1 µg of plasmid DNA (see Figures 2 and 3) in a reaction buffer of 20 mM Tris, pH 7.4, 15 mM MgCl<sub>2</sub>, 0.4 mM DTT, and 1.0 mM ATP. Reactions are initiated with extract and incubated at 30°C for 45 min.

The reaction is stopped by placing the tubes on ice and then immediately deproteinized by two phenol/chloroform (1:1) extractions. Samples are then ethanol precipitated. The nucleic acid is pelleted at 15,000 r.p.m. at 4°C for 30 min., is washed with 70% ethanol, resuspended in 50 µl H<sub>2</sub>O, and is stored at -20°C. 5 µl of plasmid from the resuspension (~100 ng) was transfected in 20 µl of DH10B cells by electroporation (400 V, 300 µF, 4 kΩ) in a Cell-Porator apparatus (Life Technologies). After electroporation, cells are transferred to a 14 ml Falcon snap-cap tube with 2 ml SOC and shaken at 37°C for 1 h. Enhancement of final kan colony counts is achieved by then adding 3 ml SOC with 10 µg/ml kanamycin and the cell suspension is shaken for a further 2 h at 37°C. Cells are then spun down at 3750 x g and the pellet is resuspended in 500 µl SOC. 200 µl is added undiluted to each of two kanamycin (50 µg/ml) agar plates and 200 µl of a 10<sup>5</sup> dilution is added to an ampicillin (100 µg/ml) plate. After overnight 37°C incubation, bacterial colonies are counted using an AccuCount 1000 (Biologics). Gene conversion effectiveness is measured as the ratio of the average of the kan colonies on both plates per amp colonies multiplied by 10<sup>-5</sup> to correct for the amp dilution.

The following procedure can also be used. 5  $\mu$ l of resuspended reaction mixtures (total volume 50  $\mu$ l) are used to transform 20  $\mu$ l aliquots of electro-competent DH10B bacteria using a Cell-Porator apparatus (Life Technologies). The mixtures are allowed to recover in 1 ml SOC at 37°C for 1 hour at which time 50  $\mu$ g/ml kanamycin or 12  $\mu$ g/ml tetracycline is added for an additional 3 hours.

5 Prior to plating, the bacteria are pelleted and resuspended in 200  $\mu$ l of SOC. 100  $\mu$ l aliquots are plated onto kan or tet agar plates and 100  $\mu$ l of a 10<sup>-4</sup> dilution of the cultures are concurrently plated on agar plates containing 100  $\mu$ g/ml of ampicillin. Plating is performed in triplicate using sterile Pyrex beads.

10 Colony counts are determined by an Accu-count 1000 plate reader (Biologics). Each plate contains 200-500 ampicillin resistant colonies or 0-500 tetracycline or kanamycin resistant colonies. Resistant colonies are selected for plasmid extraction and DNA sequencing using an ABI Prism kit on an ABI 310 capillary sequencer (PE Biosystems).

15 *Chimeric single-stranded oligonucleotides.* In Figure 1 the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (Figure 1A) 2'-O-methyl RNA nucleotides or (Figure 1B) phosphorothioate linkages. Fold changes in repair activity for correction of kan<sup>s</sup> in the HUH7 cell-free extract are presented in parenthesis. Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan<sup>s</sup> gene.

20 Molecules bearing 3, 6, 8, 10 and 12 phosphorothioate linkages in the terminal regions at each end of a backbone with a total of 24 linkages (25 bases) are tested in the kan<sup>s</sup> system. Alternatively, molecules bearing 2, 4, 5, 7, 9 and 11 in the terminal regions at each end are tested. The results of one such experiment, presented in Table 1 and Figure 1B, illustrate an enhancement of correction activity directed by some of these modified structures. In this illustrative example, the most efficient molecules contained 3 or 6 phosphorothioate linkages at each end of the 25-mer; the activities are approximately equal (molecules IX and X with results of 3.09 and 3.7 respectively). A reduction in alteration activity may 25 be observed as the number of modified linkages in the molecule is further increased. Interestingly, a single-strand molecule containing 24 phosphorothioate linkages is minimally active suggesting that this backbone modification when used throughout the molecule supports only a low level of targeted gene repair or alteration. Such a non-altering, completely modified molecule can provide a baseline control for determining efficiency of correction for a specific oligonucleotide molecule of known sequence in defining 30 the optimum oligonucleotide for a particular alteration event.

The efficiency of gene repair directed by phosphorothioate-modified, single-stranded molecules, in a length dependent fashion, led us to examine the length of the RNA modification used in

the original chimera as it relates to correction. Construct III represents the "RNA-containing" strand of chimera I and, as shown in Table 1 and Figure 2A, it promotes inefficient gene repair. But, as shown in the same figure, reducing the RNA residues on each end from 10 to 3 increases the frequency of repair. At equal levels of modification, however, 25-mers with 2'-O-methyl ribonucleotides were less effective 5 gene repair agents than the same oligomers with phosphorothioate linkages. These results reinforce the fact that an RNA containing oligonucleotide is not as effective in promoting gene repair or alteration as a modified DNA oligonucleotide.

Repair of the kanamycin mutation requires a G→C exchange. To confirm that the specific desired correction alteration was obtained, colonies selected at random from multiple 10 experiments are processed and the isolated plasmid DNA is sequenced. As seen in Figure 4, colonies generated through the action of the single-stranded molecules 3S/25G (IX), 6S/25G (X) and 8S/25G (XI) respectively contained plasmid molecules harboring the targeted base correction. While a few colonies appeared on plates derived from reaction mixtures containing 25-mers with 10 or 12 thioate linkages on both ends, the sequences of the plasmid molecules from these colonies contain nonspecific base 15 changes. In these illustrative examples, the second base of the codon is changed (see Figure 3). These results show that modified single-strands can direct gene repair, but that efficiency and specificity are reduced when the 25-mers contain 10 or more phosphorothioate linkages at each end.

In Figure 1, the numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many 20 phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the exemplified molecule although other molecules with 2, 4, 5, 7, 9 and 11 modifications at each end can also be tested. Hence oligo 12S/25G represents a 25-mer oligonucleotide which contains 12 phosphorothioate linkages on each side of the central G target mismatch base producing a fully phosphorothioate linked backbone, displayed as a dotted line. The dots are merely representative of a linkage in the figure and do not depict the actual number of linkages of the oligonucleotide. Smooth lines indicate DNA residues, wavy lines 25 indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G).

*Correction of a mutant kanamycin gene in cultured mammalian cells.* Although this portion of this example is directed to cultured mammalian cells, comparable methods may be used using cultured plant cells or protoplasts of those cells from the plant species disclosed herein. The experiments are performed using different eukaryotic cells including plant and mammalian cells, including, for example, 30 293 cells (transformed human primary kidney cells), HeLa cells (human cervical carcinoma), and H1299 (human epithelial carcinoma, non-small cell lung cancer). HeLa cells are grown at 37°C and 5% CO<sub>2</sub> in a humidified incubator to a density of 2 x 10<sup>5</sup> cells/ml in an 8 chamber slide (Lab-Tek). After replacing the

regular DMEM with Optimem, the cells are co-transfected with 10  $\mu$ g of plasmid pAURNeo(-)FIAsh and 5  $\mu$ g of modified single-stranded oligonucleotide (3S/25G) that is previously complexed with 10  $\mu$ g lipofectamine, according to the manufacturer's directions (Life Technologies). The cells are treated with the liposome-DNA-oligo mix for 6 hrs at 37°C. Treated cells are washed with PBS and fresh DMEM is 5 added. After a 16-18 hr recovery period, the culture is assayed for gene repair. The same oligonucleotide used in the cell-free extract experiments is used to target transfected plasmid bearing the kan<sup>s</sup> gene. Correction of the point mutation in this gene eliminates a stop codon and restores full expression. This expression can be detected by adding a small non-fluorescent ligand that bound to a C-C-R-E-C-C sequence in the genetically modified carboxy terminus of the kan protein, to produce a 10 highly fluorescent complex (FIAsh system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FIAsh-EDT2), cells expressing full length kan product acquire an intense green fluorescence detectable by fluorescence microscopy using a fluorescein filter set. Similar experiments are performed using the HygeGFP target as described in Example 2 with a 15 variety of mammalian cells, including, for example, COS-1 and COS-7 cells (African green monkey), and CHO-K1 cells (Chinese hamster ovary). The experiments are also performed with PG12 cells (rat pheochromocytoma) and ES cells (human embryonic stem cells).

Summary of experimental results. Tables 1, 2 and 3 respectively provide data on the efficiency of gene repair directed by single-stranded oligonucleotides. Table 1 presents data using a cell-free extract from human liver cells (Huh7) to catalyze repair of the point mutation in plasmid pkan<sup>s</sup>m4021 20 (see Figure 1). Table 2 illustrates that the oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity. Table 3 illustrates data from the repair of a frameshift mutation (Figure 3) in the tet gene contained in plasmid pTet $\Delta$ 208. Table 4 illustrates data from repair of the pkan<sup>s</sup>m4021 point mutation catalyzed by plant cell extracts prepared from canola and musa (banana). Colony numbers are presented as kan<sup>r</sup> or tet<sup>r</sup> and fold increases (single strand versus double hairpin) are presented for kan<sup>r</sup> in 25 Table 1.

Figure 5A is a confocal picture of HeLa cells expressing the corrected fusion protein from an episomal target. Gene repair is accomplished by the action of a modified single-stranded oligonucleotide containing 3 phosphorothioate linkages at each end (3S/25G). Figure 5B represents a "Z-series" of 30 HeLa cells bearing the corrected fusion gene. This series sections the cells from bottom to top and illustrates that the fluorescent signal is "inside the cells".

Results. In summary, we have designed a novel class of single-stranded oligonucleotides with backbone modifications at the termini and demonstrate gene repair/conversion

activity in mammalian and plant cell-free extracts. We confirm that the all DNA strand of the RNA-DNA double-stranded double hairpin chimera is the active component in the process of gene repair. In some cases, the relative frequency of repair by the novel oligonucleotides of the invention is elevated approximately 3-4-fold in certain embodiments when compared to frequencies directed by chimeric RNA-DNA double hairpin oligonucleotides.

This strategy centers around the use of extracts from various sources to correct a mutation in a plasmid using a modified single-stranded or a chimeric RNA-DNA double hairpin oligonucleotide. A mutation is placed inside the coding region of a gene conferring antibiotic resistance in bacteria, here kanamycin or tetracycline. The appearance of resistance is measured by genetic readout in *E.coli* grown in the presence of the specified antibiotic. The importance of this system is that both phenotypic alteration and genetic inheritance can be measured. Plasmid pK<sup>s</sup>m4021 contains a mutation (T→G) at residue 4021 rendering it unable to confer antibiotic resistance in *E.coli*. This point mutation is targeted for repair by oligonucleotides designed to restore kanamycin resistance. To avoid concerns of plasmid contamination skewing the colony counts, the directed correction is from G→C rather than G→T (wild-type). After isolation, the plasmid is electroporated into the DH10B strain of *E.coli*, which contains inactive RecA protein. The number of kanamycin colonies is counted and normalized by ascertaining the number of ampicillin colonies, a process that controls for the influence of electroporation. The number of colonies generated from three to five independent reactions was averaged and is presented for each experiment. A fold increase number is recorded to aid in comparison.

The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Patent 5,565,350, consists of two hybridized regions of a single-stranded oligonucleotide folded into a double hairpin configuration. The double-stranded targeting region is made up of a 5 base pair DNA/DNA segment bracketed by 10 base pair RNA/DNA segments. The central base pair is mismatched to the corresponding base pair in the target gene. When a molecule of this design is used to correct the kan<sup>s</sup> mutation, gene repair is observed (I in Figure 1A). Chimera II (Figure 1B) differs partly from chimera I in that only the DNA strand of the double hairpin is mismatched to the target sequence. When this chimera was used to correct the kan<sup>s</sup> mutation, it was twice as active. In the same study, repair function could be further increased by making the targeting region of the chimera a continuous RNA/DNA hybrid.

*Frame shift mutations are repaired.* By using plasmid pT<sup>s</sup>Δ208, described in Figure 1(C) and Figure 3, the capacity of the modified single-stranded molecules that showed activity in correcting a point mutation, can be tested for repair of a frameshift. To determine efficiency of correction of the mutation, a chimeric oligonucleotide (Tet I), which is designed to insert a T residue at position 208, is

used. A modified single-stranded oligonucleotide (Tet IX) directs the insertion of a T residue at this same site. Figure 3 illustrates the plasmid and target bases designated for change in the experiments. When all reaction components are present (extract, plasmid, oligomer), tetracycline resistant colonies appear. The colony count increases with the amount of oligonucleotide used up to a point beyond which the count falls off (Table 3). No colonies above background are observed in the absence of either extract or oligonucleotide, nor when a modified single-stranded molecule bearing perfect complementarity is used. Figure 3 represents the sequence surrounding the target site and shows that a T residue is inserted at the correct site. We have isolated plasmids from fifteen colonies obtained in three independent experiments and each analyzed sequence revealed the same precise nucleotide insertion. These data suggest that the single-stranded molecules used initially for point mutation correction can also repair nucleotide deletions.

*Comparison of phosphorothioate oligonucleotides to 2'-O-methyl substituted oligonucleotides.* From a comparison of molecules VII and XI, it is apparent that gene repair is more subject to inhibition by RNA residues than by phosphorothioate linkages. Thus, even though both of these oligonucleotides contain an equal number of modifications to impart nuclease resistance, XI (with 16 phosphorothioate linkages) has good gene repair activity while VII (with 16 2'-O-methyl RNA residues) is inactive. Hence, the original chimeric double hairpin oligonucleotide enabled correction directed, in large part, by the strand containing a large region of contiguous DNA residues.

*Oligonucleotides can target multiple nucleotide alterations within the same template.* The ability of individual single-stranded oligonucleotides to correct multiple mutations in a single target template is tested using the plasmid pK<sup>s</sup>m4021 and the following single-stranded oligonucleotides modified with 3 phosphorothioate linkages at each end (indicated as underlined nucleotides): Oligo1 is a 25-mer with the sequence **TTC**GATAAGCCTATGCTGACCC**G**TG corrects the original mutation present in the kanamycin resistance gene of pK<sup>s</sup>m4021 as well as directing another alteration 2 basepairs away in the target sequence (both indicated in boldface); Oligo2 is a 70-mer with the 5'-end sequence **TTC**CGGCTACGACTGGGCACAACAGACAATTGGC with the remaining nucleotides being completely complementary to the kanamycin resistance gene and also ending in 3 phosphorothioate linkages at the 3' end. Oligo2 directs correction of the mutation in pK<sup>s</sup>m4021 as well as directing another alteration 21 basepairs away in the target sequence (both indicated in boldface).

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pK<sup>s</sup>M4021 plasmid. These include, for example, a second 25-mer that alters two nucleotides that are three nucleotides apart with the sequence 5'-

TTGTGCCAGTCGTATCCGAATAGC-3'; a 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-CATCAGAGCAGCC**A**TTGTCTGTTGCCAGTCGTAGCCGAA

TAGCCTCTCCACCCAAAGCGGCCGGAGA-3'; and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-

5 GCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC**A**TTGTCTGTTGCCAGTCGTAGCCGAA  
AGCCT-3'. The nucleotides in the oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same way as the other oligonucleotides of the invention.

We assay correction of the original mutation in pK<sup>8</sup>m4021 by monitoring kanamycin  
10 resistance (the second alterations which are directed by Oligo2 and Oligo3 are silent with respect to the kanamycin resistance phenotype). In addition, in experiments with Oligo2, we also monitor cleavage of the resulting plasmids using the restriction enzyme Tsp509I which cuts at a specific site present only when the second alteration has occurred (at ATT in Oligo2). We then sequence these clones to determine whether the additional, silent alteration has also been introduced. The results of an analysis  
15 are presented below:

	Oligo1 (25-mer)	Oligo2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

20 *Nuclease sensitivity of unmodified DNA oligonucleotide.* Electrophoretic analysis of nucleic acid recovered from the cell-free extract reactions conducted here confirm that the unmodified single-stranded 25-mer did not survive incubation whereas greater than 90% of the terminally modified oligos did survive (as judged by photo-image analyses of agarose gels).

*Plant extracts direct repair.* The modified single-stranded constructs can be tested in plant cell extracts. We have observed gene alteration using extracts from multiple plant sources, including, for example, Arabidopsis, tobacco, banana, maize, soybean, canola, wheat, spinach as well as spinach chloroplast extract or extracts made from other plant cells disclosed herein. We prepare the extracts by grinding plant tissue or cultured cells under liquid nitrogen with a mortar and pestle. We extract 3 ml of the ground plant tissue with 1.5 ml of extraction buffer (20 mM HEPES, pH7.5; 5 mM KCl;

1.5 mM MgCl<sub>2</sub>; 10 mM DTT; and 10% [v/v] glycerol). Some plant cell-free extracts also include about 1% (w/v) PVP. We then homogenize the samples with 15 strokes of a Dounce homogenizer. Following homogenization, we incubate the samples on ice for 1 hour and centrifuge at 3000 x g for 5 minutes to remove plant cell debris. We then determine the protein concentration in the supernatants (extracts) by

5 Bradford assay. We dispense 100 µg (protein) aliquots of the extracts which we freeze in a dry ice-ethanol bath and store at -80°C.

We describe experiments using two sources here: a dicot (canola) and a monocot (banana, *Musa acuminata* cv. Rasthali). Each vector directs gene repair of the kanamycin mutation (Table 4); however, the level of correction is elevated 2-3 fold relative to the frequency observed with the 10 chimeric oligonucleotide. These results are similar to those observed in the mammalian system wherein a significant improvement in gene repair occurred when modified single-stranded molecules were used.

Tables are attached hereto.

Table I

*Gene repair activity is directed by single-stranded oligonucleotides.*

Oligonucleotide	Plasmid	Extract (ug)	kan' colonies	Fold increase
I	pK <sup>S</sup> m4021	10	300	
I		20	418	1.0x
II		10	537	
II		20	748	1.78x
III		10	3	
III		20	5	0.01x
IV		10	112	
IV		20	96	0.22x
V		10	217	
V		20	342	0.81x
VI		10	6	
VI		20	39	0.093x
VII		10	0	
VII		20	0	0x
VIII		10	3	
VIII		20	5	0.01x
IX		10	936	
IX		20	1295	3.09x
X		10	1140	
X		20	1588	3.7x
XI		10	480	
XI		20	681	1.6x
XII		10	18	
XII		20	25	0.059x
XIII		10	0	
XIII		20	4	0.009x
I		20	0	
I		-	0	

Plasmid pK<sup>S</sup>m4021 (1 $\mu$ g), the indicated oligonucleotide (1.5  $\mu$ g chimeric oligonucleotide or 0.55  $\mu$ g single-stranded oligonucleotide; molar ratio of oligo to plasmid of 360 to 1) and either 10 or 20  $\mu$ g of HUH7 cell-free extract were incubated 45 min at 37°C. Isolated plasmid DNA was electroporated into *E. coli* (strain DH10B) and the number of kan' colonies counted. The data represent the number of kanamycin resistant colonies per 10<sup>6</sup> ampicillin resistant colonies generated from the same reaction and is the average of three

experiments (standard deviation usually less than +/- 15%). Fold increase is defined relative to 418 kan' colonies (second reaction) and in all reactions was calculated using the 20 $\mu$ g sample.

Table II

*Modified single-stranded oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity.*

A. <u>Oligonucleotide</u>	<u>Plasmid</u>	<u>Extract</u>	<u>kan<sup>r</sup> colonies</u>
IX (3S/25G)		HUH7	637
X (6S/25G)		HUH7	836
IX		MEF2 <sup>+</sup>	781
X		MEF2 <sup>+</sup>	676
IX		MEF3 <sup>+</sup>	582
X		MEF3 <sup>+</sup>	530
IX		MEF <sup>++</sup>	332
X		MEF <sup>++</sup>	497
-		MEF2 <sup>+</sup>	10
-		MEF3 <sup>+</sup>	5
-		MEF <sup>++</sup>	14

Chimeric oligonucleotide (1.5  $\mu$ g) or modified single-stranded oligonucleotide (0.55  $\mu$ g) was incubated with 1  $\mu$ g of plasmid pK<sup>m</sup>4021 and 20  $\mu$ g of the indicated extracts. MEF represents mouse embryonic fibroblasts with either MSH2 (2<sup>+</sup>) or MSH3 (3<sup>+</sup>) deleted. MEF<sup>++</sup> indicates wild-type mouse embryonic fibroblasts. The other reaction components were then added and processed through the bacterial readout system. The data represent the number of kanamycin resistant colonies per  $10^6$  ampicillin resistant colonies.

Table III

*Frameshift mutation repair is directed by single-stranded oligonucleotides*

Oligonucleotide	Plasmid	Extract	<i>tet</i> <sup>r</sup> colonies
Tet IX (3S/25A; 0.5 µg)	pT <sup>r</sup> Δ208 (1µg)	-	0
-	-	20µg	0
Tet IX (0.5 µg)	-	-	48
Tet IX (1.5 µg)	-	-	130
Tet IX (2.0 µg)	-	-	68
Tet I (chimera; 1.5 µg)	-	-	48

Each reaction mixture contained the indicated amounts of plasmid and oligonucleotide.

The extract used for these experiments came from HUH7 cells. The data represent the number of tetracycline resistant colonies per  $10^6$  ampicillin resistant colonies generated from the same reaction and is the average of 3 independent experiments. Tet I is a chimeric oligonucleotide and Tet IX is a modified single-stranded oligonucleotide that are designed to insert a T residue at position 208 of pT<sup>r</sup>Δ208. These oligonucleotides are equivalent to structures I and IX in Figure 2.

Table IV

*Plant cell-free extracts support gene repair by single-stranded oligonucleotides*

Oligonucleotide	Plasmid	Extract	kan <sup>r</sup> colonies
II (chimera)	pK <sup>S</sup> m4021	30µg Canola	337
IX (3S/25G)		Canola	763
X (6S/25G)		Canola	882
II		<i>Musa</i>	203
IX		<i>Musa</i>	343
X		<i>Musa</i>	746
-		Canola	0
-		<i>Musa</i>	0
IX		- Canola	0
X		- <i>Musa</i>	0

Canola or *Musa* cell-free extracts were tested for gene repair activity on the kanamycin-sensitive gene as previously described in (18). Chimeric oligonucleotide II (1.5 µg) and modified single-stranded oligonucleotides IX and X (0.55µg) were used to correct pK<sup>S</sup>m4021. Total number of kan<sup>r</sup> colonies are present per 10<sup>7</sup> ampicillin resistant colonies and represent an average of four independent experiments.

## Table V

*Gene repair activity in cell-free extracts prepared from yeast (*Saccharomyces cerevisiae*)*

Cell-type	Plasmid	Chimeric Oligo	SS Oligo	kan' /amp' x 10 <sup>6</sup>
Wild type	pKan'm4021	1 $\mu$ g	1 $\mu$ g	0.36
Wild type		1 $\mu$ g	1 $\mu$ g	0.81
$\Delta$ RAD52				10.72
$\Delta$ RAD52				17.41
$\Delta$ PMS1		1 $\mu$ g	1 $\mu$ g	2.02
$\Delta$ PMS1				3.23

In this experiment, the kan' gene in pKan'4021 is corrected by either a chimeric double-hairpin oligonucleotide or a single-stranded oligonucleotide containing three thioate linkages at each end (3S/2SG).

**EXAMPLE 2**  
**Yeast Cell Targeting Assay Method for Base**  
**Alteration and Preferred Oligonucleotide Selection**

In this example, single-stranded oligonucleotides with modified backbones and double-hairpin oligonucleotides with chimeric, RNA-DNA backbones are used to measure gene repair using two episomal targets with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair. These plasmids are pAURHYG(rep)GFP, which contains a point mutation in the hygromycin resistance gene (Figure 7), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (Figure 7) and pAURHYG(Δ)GFP which has a single base deletion. We also use the 5 plasmid containing a wild-type copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)GFP, as a control. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, at codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In 10 pAURHYG(ins)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, at codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting 15 a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene.

We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, 20 pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)EGFP and ligation into pAUR123 (Panvera, CA). We digest 10 µg pAUR123 vector DNA, as well 25 as, 10 µg of each pHyg(x)EGFP construct with KpnI and SalI (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify using a Qiagen maxiprep kit.

We use this system to assay the ability of five oligonucleotides (shown in Figure 8) to 30 support correction under a variety of conditions. The oligonucleotides which direct correction of the mutation in pAURHYG(rep)GFP can also direct correction of the mutation in pAURHYG(ins)GFP. Three of the four oligonucleotides (HygE3T/25, HygE3T/74 and HygGG/Rev) share the same 25-base sequence surrounding the base targeted for alteration. HygGG/Rev is an RNA-DNA chimeric double hairpin

oligonucleotide of the type described in the prior art. One of these oligonucleotides, HygE3T/74, is a 74-base oligonucleotide with the 25-base sequence centrally positioned. The fourth oligonucleotide, designated HygE3T/74 $\alpha$ , is the reverse complement of HygE3T/74. The fifth oligonucleotide, designated Kan70T, is a non-specific, control oligonucleotide which is not complementary to the target sequence.

5 Alternatively, an oligonucleotide of identical sequence but lacking a mismatch to the target or a completely thioate modified oligonucleotide or a completely 2'-O-methylated modified oligonucleotide may be used as a control. Alternatively, oligonucleotides containing one, two, three, four, five, six, eight, ten or more LNA modifications on at least one of the two termini (and preferably the 3' terminus) may be used in different embodiments.

10 *Oligonucleotide synthesis and cells.* We synthesized and purified the chimeric, double-hairpin oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) as described in Example 1. Plasmids used for assay were maintained stably in yeast (*Saccharomyces cerevisiae*) strain LSY678 MAT $\alpha$  at low copy number under aureobasidin selection.

15 Plasmids and oligonucleotides are introduced into yeast cells by electroporation as follows: to prepare electrocompetent yeast cells, we inoculate 10 ml of YPD media from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We then add 30 ml of fresh YPD media to the overnight cultures and continue shaking at 30°C until the OD<sub>600</sub> was between 0.5 and 1.0 (3-5 hours). We then wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We then centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml

20 ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120  $\mu$ l 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40  $\mu$ l of cells with 5  $\mu$ g of nucleic acid, unless otherwise stated, and incubate on ice for 5 minutes.

25 We then transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25  $\mu$ F, 200  $\Omega$  for one five-second pulse. We then immediately resuspend the cells in 1 ml YPD supplemented with 1M sorbitol and incubate the cultures at 30°C with shaking at 300 rpm for 6 hours. We then spread 200  $\mu$ l of this culture on selective plates containing 300  $\mu$ g/ml hygromycin and spread 200  $\mu$ l of a 10<sup>5</sup> dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We then count the colonies on the plates and calculate the gene conversion efficiency by determining the number

30 of hygromycin resistance colonies per 10<sup>5</sup> aureobasidinA resistant colonies.

*Frameshift mutations are repaired in yeast cells.* We test the ability of the oligonucleotides shown in Figure 8 to correct a frameshift mutation *in vivo* using LSY678 yeast cells

containing the plasmid pAURHYG(ins)GFP. These experiments, presented in Table 6, indicate that these oligonucleotides can support gene correction in yeast cells. These data reinforce the results described in Example 1 indicating that oligonucleotides comprising phosphorothioate linkages facilitate gene correction much more efficiently than control duplex, chimeric RNA-DNA oligonucleotides. This gene correction 5 activity is also specific as transformation of cells with the control oligonucleotide Kan70T produced no hygromycin resistant colonies above background and thus Kan70T did not support gene correction in this system. In addition, we observe that the 74-base oligonucleotide (HygE3T/74) corrects the mutation in pAURHYG(ins)GFP approximately five-fold more efficiently than the 25-base oligonucleotide 10 (HygE3T/25). We also perform control experiments with LSY678 yeast cells containing the plasmid pAURHYG(wt)GFP. With this strain we observed that even without added oligonucleotides, there are too many hygromycin resistant colonies to count.

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pAURHYG(x)eGFP plasmid. These include, for example, one that alters two basepairs that are 3 nucleotides apart is a 74-mer with the sequence 5'-  
15 CTCGTCTTCAGCTTCGATGTAGGAGGGCGTGG**TAC****CGTC**CCTGCGGGTAAATAGCTGCGCCGATG  
GTTTCTAC-3'; a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-  
CTCGTCTTCAGCTTCGATGTAGGAGGGCGTGG**ATAC****CGTC**CCTGCGGGTAA**AC**AGCTGCGCCGATG  
GTTTCTAC-3'; and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-  
20 CTCGTCTTCAGCTTCGATGTAGGAGGGCGTGG**ATAC****CGTC**CCTGCGGGTAAATAGCTGCGCCG**ACG**  
GTTTCTAC. The nucleotides in these oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same ways as the other oligonucleotides of the invention.

*Oligonucleotides targeting the sense strand direct gene correction more efficiently.* We compare the ability of single-stranded oligonucleotides to target each of the two strands of the target 25 sequence of both pAURHYG(ins)GFP and pAURHYG(rep)GFP. These experiments, presented in Tables 7 and 8, indicate that an oligonucleotide, HygE3T/74 $\alpha$ , with sequence complementary to the sense strand (i.e. the strand of the target sequence that is identical to the mRNA) of the target sequence facilitates gene correction approximately ten-fold more efficiently than an oligonucleotide, HygE3T/74, with sequence complementary to the non-transcribed strand which serves as the template for the 30 synthesis of RNA. As indicated in Table 7, this effect was observed over a range of oligonucleotide concentrations from 0-3.6  $\mu$ g, although we did observe some variability in the difference between the two oligonucleotides (indicated in Table 7 as a fold difference between HygE3T/74 $\alpha$  and HygE3T/74).

Furthermore, as shown in Table 8, we observe increased efficiency of correction by HygE3T/74 $\alpha$  relative to HygE3T/74 regardless of whether the oligonucleotides were used to correct the base substitution mutation in pAURHYG(rep)GFP or the insertion mutation in pAURHYG(ins)GFP. The data presented in Table 8 further indicate that the single-stranded oligonucleotides correct a base substitution mutation more efficiently than an insertion mutation. However, this last effect was much less pronounced and the oligonucleotides of the invention are clearly able efficiently to correct both types of mutations in yeast cells. In addition, the role of transcription is investigated using plasmids with inducible promoters such as that described in Figure 10.

*Optimization of oligonucleotide concentration.* To determine the optimal concentration of oligonucleotide for the purpose of gene alteration, we test the ability of increasing concentrations of Hyg3T/74 $\alpha$  to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678. We chose this assay system because our previous experiments indicated that it supports the highest level of correction. However, this same approach could be used to determine the optimal concentration of any given oligonucleotide. We test the ability of Hyg3T/74 $\alpha$  to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678 over a range of oligonucleotide concentrations from 0-10.0  $\mu$ g. As shown in Table 9, we observe that the correction efficiency initially increases with increasing oligonucleotide concentration, but then declines at the highest concentration tested.

Tables are attached hereto.

Table 6

Correction of an insertion mutation in *pAURHYG(ins)GFP* by *HygGG/Rev*, *HygE3T/25* and *HygE3T/74*

Oligonucleotide Tested	Colonies on Hygromycin	Colonies on Aureobasidin (/10 <sup>5</sup> )	Correction Efficiency
HygGG/Rev	3	157	0.02
HygE3T/25	64	147	0.44
HygE3T/74	280	174	1.61
Kan70T	0	—	—

Table 7

An oligonucleotide targeting the sense strand of the target sequence corrects more efficiently.

Amount of Oligonucleotide (μg)	Colonies per hygromycin plate	
	HygE3T/74	HygE3T/74α
0	0	0
0.6	24	128 (8.4x)*
1.2	69	140 (7.5x)*
2.4	62	167 (3.8x)*
3.6	29	367 (15x)*

\* The numbers in parentheses represent the fold increase in efficiency for targeting the non-transcribed strand as compared to the other strand of a DNA duplex that encodes a protein.

Table 8

*Correction of a base substitution mutation is more efficient than correction of a frame shift mutation.*

Oligonucleotide Tested (5 µg)	Plasmid tested (contained in LSY678)	
	pAURHYG(ins)GFP	pAURHYG(rep)GFP
HygE3T/74	72	277
HygE3T/74α	1464	2248
Kan70T	0	0

Table 9

*Optimization of oligonucleotide concentration in electroporated yeast cells.*

Amount (µg)	Colonies on hygromycin	Colonies on aureobasidin (/10 <sup>5</sup> )	Correction efficiency
0	0	67	0
1.0	5	64	0.08
2.5	47	30	1.57
5.0	199	33	6.08
7.5	383	39	9.79
10.0	191	33	5.79

### Example 3

#### Cultured Cell Manipulation

Although disclosure in this example is directed to use of stem cells or human blood cells and microinjection, the microinjection procedures may also be used with cultured plant cells or protoplasts using any plant species, including those disclosed herein. Mononuclear cells are isolated from human umbilical cord blood of normal donors using Ficoll Hypaque (Pharmacia Biotech, Uppsala, Sweden) density centrifugation. CD34+ cells are immunomagnetically purified from mononuclear cells using either

the progenitor or Multisort Kits (Miltenyi Biotec, Auburn, CA). Lin<sup>-</sup>CD38<sup>-</sup> cells are purified from the mononuclear cells using negative selection with StemSep system according to the manufacturer's protocol (Stem Cell Technologies, Vancouver, CA). Cells used for microinjection are either freshly isolated or cryopreserved and cultured in Stem Medium (S Medium) for 2 to 5 days prior to microinjection.

5 S Medium contains Iscoves' Modified Dulbecco's Medium without phenol red (IMDM) with 100 µg/ml glutamine/penicillin/streptomycin, 50 mg/ml bovine serum albumin, 50 µg/ml bovine pancreatic insulin, 1 mg/ml human transferrin, and IMDM (Stem Cell Technologies), 40 µg/ml low-density lipoprotein (LDL; Sigma, St. Louis, MO), 50 mM HEPES buffer and 50 µM 2-mercaptoethanol, 20 ng/ml each of thrombopoietin, flt-3 ligand, stem cell factor and human IL-6 (Pepro Tech Inc., Rocky Hill, NJ). After 10 microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

15 35 mm dishes are coated overnight at 4° C with 50 µg/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, WI) in phosphate buffered saline and washed with IMDM containing glutamine/penicillin/streptomycin. 300 to 2000 cells are added to cloning rings and attached to the plates for 45 minutes at 37° C prior to microinjection. After incubation, cloning rings are removed and 2 ml of S Medium are added to each dish for microinjection. Pulled injection needles with a range of 0.22 µm to 0.3 µm outer tip diameter are used. Cells are visualized with a microscope equipped with a temperature controlled stage set at 37° C and injected using an electronically interfaced Eppendorf Micromanipulator and Transector. Successfully injected cells are intact, alive and remain attached to the plate post injection. Molecules that are fluorescently labeled allow determination of the amount of 20 oligonucleotide delivered to the cells.

25 For *in vitro* erythropoiesis from Lin<sup>-</sup>CD38<sup>-</sup> cells, the procedure of Malik, 1998 can be used. Cells are cultured in ME Medium for 4 days and then cultured in E Medium for 3 weeks. Erythropoiesis is evident by glycophorin A expression as well as the presence of red color representing the presence of hemoglobin in the cultured cells. The injected cells are able to retain their proliferative capacity and the ability to generate myeloid and erythroid progeny. CD34+ cells can convert a normal A ( $\beta^A$ ) to sickle T ( $\beta^S$ ) mutation in the  $\beta$ -globin gene or can be altered using any of the oligonucleotides of the invention herein for correction or alteration of a normal gene to a mutant gene. Alternatively, stem cells can be isolated from blood of humans having genetic disease mutations and the oligonucleotides of the invention can be used to correct a defect or to modify genomes within those cells.

30 Alternatively, non-stem cell populations of cultured cells can be manipulated using any method known to those of skill in the art including, for example, the use of polycations, cationic lipids,

liposomes, polyethylenimine (PEI), electroporation, biolistics, calcium phosphate precipitation, or any other method known in the art.

Biostatic delivery of oligonucleotide into plant cells may be accomplished according to the following method. One milliliter of packed cell volume of plant cell suspensions are subcultured onto plates containing solid medium [with Murashige and Skoog salts from Gibco/BRL, 500 mg/liter Mes, 1 mg/liter thiamin, 100 mg/liter myo-inositol, 180 mg/liter KH<sub>2</sub>PO<sub>4</sub>, 2.21 mg/liter 2,4-dichlorophenoxyacetic acid (2,4-D), and 30 g/liter sucrose (pH 5.7) and having 8 g/liter agar-agar from Sigma added before autoclaving]. By using a helium-driven particle gun such as that from BioRad and following manufacturers directions, oligonucleotides may be introduced to cells after precipitation onto 1 micrometer or comparable gold microcarriers (Bio-Rad). To precipitate onto microcarriers, 35 microliters of a particle suspension (60 mg of microcarriers per ml of 100% ethanol) is transferred to a 1.5 ml microcentrifuge tube, which is agitated on a vortex mixer. Then 40 microliter of resuspended oligonucleotide (60 ng/microliter water) is added; then 75 microliter of ice-cold 2.5 M CaCl<sub>2</sub> is added; then 75 microliter of ice-cold 0.1 M spermidine is added. The tube is mixed vigorously or a vortex mixer for 10 min at room temperature. The particles are allowed to settle for 10 min and are centrifuged at 11,750 g for 30 sec. The supernatant is removed and the particles are resuspended in 50 microliter of 100% ethanol. An aliquot of 10 microliter of the resuspended particles are applied to each macro-projectile which is used to bombard each plate once at 900 psi (1 psi = 6.89 kPa) with a gap distance (distance from power source to macroprojectile) of 1 cm and a target distance (distance from microprojectile launch site to target material) of 10 cm.

An alternative method of delivery can be used as follows. Cultured cells are suspended in liquid N6 medium and then plated on a VWR Scientific glass fiber filter. About 0.4 microgram of oligonucleotide are precipitated with 15 microliter of 2.5 mM CaCl<sub>2</sub> and 5 microliter of 0.1 M spermidine onto 25 microgram of 1.0 micrometer gold particles. Microprojectile bombardment is performed by using a Bio-Rad PDS-1000 He particle delivery system or comparable machine following manufacturers instructions. Alterations in oligonucleotide concentrations can be employed to determine the optimum concentration of oligonucleotide according to the procedures described herein for any particular oligonucleotide of the invention.

Alternatively, the oligonucleotide of the invention may be delivered to a plant cell by electroporation of a protoplast derived from a plant part. The protoplasts may be formed by enzymatic treatment of a plant part, particularly a leaf, according to techniques such as those in Gallois et al., Methods in Molecular Biology 55: 89-107 by Humana Press. Such conditions for electroporation use

about  $3 \times 10^5$  protoplasts in a total volume of about 0.3 ml with a concentration of oligonucleotide of between 0.6 to 4 microgram per ml.

#### EXAMPLE 4

##### Plant Cells

5           The oligonucleotides of the invention can also be used to repair or direct a mutagenic event in plants and animal cells. Although little information is available on plant mutations amongst natural cultivars, the oligonucleotides of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying Gln can be modified at a specific site to TAA; a AAG codon specifying Lys can be modified to UAG at a specific 10 site; and a CGA codon for Arg can be modified to a UGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a defective truncated protein, shortened at the site of the stop codon

15           Alternatively, frameshift additions or deletions can be directed into the genome at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

20           For introduction of a T-DNA, including the T-DNA in the plasmid of Figure 11, into a plant cell, *Agrobacterium tumefaciens* is used. These techniques are routine standard techniques known in the art. For example, one method follows. We transform *A. tumefaciens* is transformed by electroporation (using a BioRad Gene Pulser™). Competent *A. tumefaciens* is prepared using a method similar to that of preparing competent *E. coli* by suspending a freshly grown culture three times in ice-cold water and a final resuspension in 10% glycerol. Electroporation conditions are a 0.2 cm gap cuvette at a setting of 25  $\mu$ F, 200  $\Omega$  and 2.5 kV.

25           *A. tumefaciens* containing a plasmid with a T-DNA is then used to introduce the T-DNA into a plant cell using routine standard techniques known in the art. For example, we transform *Arabidopsis* by vacuum infiltration or by dipping flowers in an Agrobacterium solution containing a surfactant, e.g. L-77. Seeds are then collected, grown and screened for presence of the T-DNA. Alternatively, Agrobacterium can be used to transform callus tissue and the callus tissue can then be used to regenerate transformed plants.

30           All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some

detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

5 **Notes on the tables presented below:**

Each of the following tables presents, for the specified gene, a plurality of mutations that are known to confer a relevant phenotype and, for each mutation, the oligonucleotides that can be used to correct the respective mutation site-specifically in the genome according to the present invention.

10 The left-most column identifies each alteration or mutation and the phenotype that the alteration/mutation confers.

15 For most entries, the mutation/alteration is identified at both the nucleic acid and protein level. At the amino acid level, mutations are presented according to the following standard nomenclature. The centered number identifies the position of the mutated codon in the protein sequence; to the left of the number is the wild type residue and to the right of the number is the mutant codon. Terminator codons are shown as "TERM". At the nucleic acid level, the entire triplet of the wild type and mutated codons is shown.

20 The middle column presents, for each mutation, four oligonucleotides capable of repairing the mutation site-specifically in the genome or in cloned DNA including DNA in artificial chromosomes, episomes, plasmids, or other types of vectors. The oligonucleotides of the invention, however, may include any of the oligonucleotides sharing portions of the sequence of the 121 base sequence. Thus, oligonucleotides of the invention for each of the depicted targets may be 18, 19, 20 up to about 121 nucleotides in length. Sequence may be added non-symmetrically.

25 All oligonucleotides are presented, per convention, in the 5' to 3' orientation. The nucleotide that effects the change in the genome is underlined and presented in bold.

30 The first of the four oligonucleotides for each mutation is a 121 nt oligonucleotide centered about the repair/altering nucleotide. The second oligonucleotide, its reverse complement, targets the opposite strand of the DNA duplex for repair/alteration. The third oligonucleotide is the minimal 17 nt domain of the first oligonucleotide, also centered about the repair/alteration nucleotide. The fourth oligonucleotide is the reverse complement of the third, and thus represents the minimal 17 nt domain of the second.

The third column of each table presents the SEQ ID NO: of the respective repair oligonucleotide.

**Example 5****Engineering herbicide resistant plants**

Chemical weed control is an important tool of modern agriculture and many herbicides have been developed for this purpose. Their use has resulted in substantial increases in the yields of many crops, including, for example, maize, soybeans, and cotton. Thus while the use of fertilizers and new high-yielding crop varieties have contributed greatly to the "green revolution," chemical weed control has also been at the forefront of technological achievement.

Herbicides having broad-spectrum activity are particularly useful because they obviate the need for multiple herbicides targeting different classes of weeds. The problem with such herbicides is that they typically also affect crops which are exposed to the herbicide. One way to overcome this is to generate plants which are resistant to one or more broad-spectrum herbicides. Such herbicide-tolerant plants may reduce the need for tillage to control weeds, thereby effectively reducing soil erosion and can reduce the quantity and number of different herbicides applied in the field.

Common herbicides used, for example, include those that inhibit the enzyme 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS), for example N-phosphonomethyl-glycine (e.g. glyphosate), those that inhibit acetolactate synthase (ALS) activity, for example the sulfonylureas and related herbicides, and those that inhibit dihydropteroate synthase, for example methyl[(4-amino-phenyl)sulfonyl]carbamate (e.g. Asulam). Herbicide-tolerant plants can be produced by several methods, including, for example, introducing into the genome of the plant the ability to degrade the herbicide, the capacity to produce a higher level of the targeted enzyme, and/or expressing an herbicide-tolerant allele of the enzyme.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes that confer herbicide resistance.

**Table 10**  
**Genome-Altering Oligos Conferring Glyphosate Resistance**

5 Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
10 5 Glyphosate Resistance EPSPS <i>Arabidopsis thaliana</i> Gly97Ala GGC-GCC	AAGCGTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTC TTATTAAGCTTCTGCCTCCAAGTCTCTATCAAATCGGATCCTGC	4341
	TTCTCGCTGCTCTGCTGAGGTATATACAC GTGATATATACCTCAGACAGAGCAGCGAGAAGCAGGATCCGATT	4342
	TGATAGAGACTTGGAGGCAGGAAGCTTAATAAGACCGGAGATT	4343
	CTCTAATGGGTTGAAGTACAATCTCGACGCTT	4344
15 10 5 Glyphosate Resistance EPSPS <i>Brassica napus</i> Gly93Ala GGA-GCA	AAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGGTC TCATTAAGCTACCCGATCCAAATCTCTCCAATCGGATCCTCC	4345
	TTCTTGCGCTCTATCTGAGGTACATATACT	
	AGTATATGTACCTCAGATAGAGCGGCAAGAAGGAGGATCCGATT GGAGAGAGATTGGATGCGGGTAGCTTAATGAGACCCGAGATT	4346
	CTCTGATTGGGTTGAAGCACAATCTCTGAAGCTT	
	GCTACCCGATCCAAAT	4347
20 15 5 Glyphosate Resistance EPSPS 1 <i>Nicotiana tabacum</i> Gly95Ala GGT-GCT	ATTGGATGCGGGTAGC AGCCCACGAGATTGTGCTGCAACCCATCAAAGATATATCAGGC	4348
	ACTGTTAAATTGCCTGCTTCTAAATCCCTTCCAATCGTATTCTCC	
	TTCTTGCTGCCCTTCTAAGGGAAAGGACTGT	
	ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAACGATT GGAAAGGGATTAGAACAGCAGGCAATTAAACAGTGCCTGATATATC	4349
	TTTGATGGGTTGCAGCACAATCTCGTTGGGCT	
25 20 5 Glyphosate Resistance EPSPS 2 <i>Nicotiana tabacum</i> Gly62Ala GGA-GCA	ATTGCCTGCTTCTAAAT	4351
	ATTAGAACAGGCAAT	4352
	ATTGTTTCTTGGTACGAAATGTCCTCCTGTTCGAATTGTCAGCA AGGGAGGCCCTCCCGCAGGGAAAGGTAAAGCTCTGGATCAATT	4353
	AGCAGCCAGTACTGACTGCTCTGCTTATGGC	
	GCCATAAGCAGAGCAGTCAGTACTGGCTGCTAATTGATCCAGA GAGCTTACCTCCCTGCGGGAAAGGCCCTCCCTGCTGACAATT	4354
30 25 5 Glyphosate Resistance EPSPS <i>Zea mays</i> Gly168Ala GGT-GCT	GAACAGGAGGACATTTCGTACCAAGGAAACAAT	
	CCTTCCCGAGGGAGG	4355
	CCTTCCCTGCGGGAGG	4356
30 30 5 Glyphosate Resistance EPSPS <i>Zea mays</i> Gly168Ala GGT-GCT	ATTGTTTCTTGGCACTGACTGCCACCTGTTGTCATGGAA TCGGAGGGCTACCTGCTGGCAAGGTCAAGCTGCTGGCTCCATC	4357
	AGCAGTCAGTACTTGAGTGCCCTGCTGATGGC GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGA	4358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GCTACCT <u>G</u> GGCAAGG	4359
	CCTTGCC <u>A</u> G <u>C</u> AGGTAGC	4360
5 Glyphosate Resistance EPSPS <i>Oryza sativa</i> Gly115Ala GGT-GCT	ACTGTTCC <u>T</u> GGCACTGAATGCCACCTG <u>T</u> GT <u>G</u> CAAGGGAA ATTGGAGGA <u>C</u> TT <u>C</u> T <u>G</u> <u>C</u> GGCAAGGTTAAGCTCTGGTTCCAT CAGCAGTCAGTACTTGAGTG <u>C</u> CTGCTGATGGC GCCATCAGCAAGGACTCAAGTACTGACTGCTGATGGAACCAGA GAGCTTAACCTTGCC <u>A</u> GGCAGGAAGTCCTCCAATTCCCTGACAC GAACAGGTGGGCATT <u>C</u> AGT <u>G</u> CCAAGGAAACAGT ACTTC <u>C</u> T <u>G</u> GGCAAGG	4361 4362 4363 4364
10 Glyphosate Resistance EPSPS <i>Petunia x hybrida</i> Gly93Ala GGC-GCC	AGCCTTCTGAGATAGTGTGCAACCCATTAAAGAGAT <u>T</u> CA <u>G</u> GGCA CTGTTAAATTGCCT <u>G</u> C <u>C</u> CTCTAA <u>T</u> ATT <u>C</u> ATT <u>T</u> CTAA <u>T</u> AGAATT <u>T</u> CCCT TCTTGCTGC <u>C</u> TT <u>T</u> CTGAAGGAA <u>C</u> ACTGT ACAGTT <u>G</u> CC <u>T</u> TC <u>A</u> G <u>A</u> TA <u>A</u> GG <u>C</u> AG <u>C</u> AA <u>A</u> GG <u>G</u> AA <u>A</u> TT <u>T</u> ATT <u>A</u> GATAAT <u>G</u> ATT <u>T</u> AG <u>G</u> GG <u>C</u> AG <u>G</u> CA <u>T</u> TA <u>A</u> CA <u>G</u> T <u>G</u> CT <u>G</u> AA <u>A</u> TT <u>T</u> CT TTAATGGGTG <u>C</u> AA <u>C</u> ACT <u>T</u> CT <u>C</u> AG <u>A</u> GG <u>G</u> CT ATT <u>G</u> C <u>T</u> GC <u>C</u> CT <u>T</u> CTAA <u>A</u> AT <u>T</u> TA <u>G</u> AG <u>G</u> GG <u>C</u> AG <u>G</u> CA <u>A</u> T	4365 4366 4367 4368
15 Glyphosate Resistance EPSPS <i>Lycopersicon esculentum</i> Gly97Ala GGT-GCT	AACCCC <u>A</u> T <u>G</u> AG <u>A</u> T <u>T</u> GT <u>G</u> CT <u>A</u> GN <u>A</u> CC <u>C</u> AT <u>C</u> AA <u>A</u> GA <u>T</u> AT <u>A</u> T <u>T</u> GG <u>T</u> CTGTTAAATT <u>A</u> CC <u>C</u> G <u>T</u> CG <u>A</u> AT <u>C</u> C <u>T</u> TT <u>C</u> CA <u>A</u> TC <u>G</u> T <u>A</u> TT <u>T</u> CC <u>C</u> TCTTGCTGC <u>C</u> CC <u>T</u> TT <u>T</u> CT <u>G</u> AG <u>GG</u> GA <u>AG</u> GA <u>CT</u> GT ACAGTC <u>C</u> TT <u>C</u> C <u>T</u> CA <u>G</u> AA <u>A</u> GG <u>G</u> C <u>A</u> GA <u>A</u> GG <u>G</u> AA <u>A</u> TC <u>G</u> ATT GG <u>A</u> AA <u>GG</u> GA <u>TT</u> <u>T</u> CG <u>A</u> AG <u>C</u> GG <u>G</u> TA <u>AT</u> <u>T</u> AA <u>C</u> AG <u>T</u> AC <u>C</u> CA <u>G</u> AT <u>A</u> T <u>A</u> TTTGATGGGTN <u>T</u> AC <u>G</u> CA <u>A</u> AT <u>T</u> CT <u>C</u> AT <u>GG</u> GT ATT <u>A</u> CC <u>C</u> G <u>T</u> CG <u>A</u> AT AT <u>T</u> TC <u>G</u> AA <u>G</u> CG <u>GG</u> TA <u>AT</u>	4369 4370 4371 4372
20 Glyphosate Resistance EPSPS <i>Lolium rigidum</i> Gly107Ala GGT-GCT	ATTGTTCC <u>T</u> GGCACTGA <u>T</u> CTGCCACCTG <u>T</u> CG <u>K</u> AT <u>C</u> A <u>CG</u> GG <u>C</u> A TTGGAGGG <u>C</u> TAC <u>C</u> T <u>G</u> <u>C</u> GG <u>C</u> AA <u>G</u> GT <u>T</u> AA <u>G</u> CT <u>G</u> T <u>C</u> GG <u>T</u> CC <u>C</u> AT <u>C</u> AG <u>C</u> AG <u>C</u> CA <u>A</u> AT <u>A</u> CT <u>T</u> GA <u>G</u> T <u>T</u> CC <u>T</u> GT <u>G</u> AT <u>GG</u> C GCCATCAG <u>C</u> AG <u>A</u> GG <u>A</u> ACT <u>C</u> A <u>G</u> T <u>A</u> T <u>T</u> GG <u>C</u> T <u>G</u> AT <u>G</u> GA <u>AC</u> CA <u>G</u> A CAGCTTAAC <u>C</u> TT <u>G</u> CC <u>A</u> GG <u>T</u> AG <u>C</u> CC <u>T</u> CCA <u>A</u> T <u>G</u> CC <u>G</u> T <u>T</u> GT <u>C</u> G AACAGGTGG <u>C</u> AG <u>T</u> CA <u>G</u> T <u>G</u> CCA <u>A</u> GG <u>A</u> ACA <u>A</u> T GCTACCT <u>G</u> GG <u>C</u> AG <u>G</u> CCTTGCC <u>A</u> G <u>C</u> AG <u>G</u> T <u>AG</u> C	4373 4374 4375 4376

**Table 11**  
**Genome-Altering Oligos Conferring Imidazolinone and Sulfonlurea Herbicide Resistance**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Sulfonlurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Ser CCT-TCT	AGCGGATTAGCCGATGCGTTAGATAGTGTCTCTTAGCA ATCACAGGACAAGTC <u>T</u> CTCGTCGTATGATTGGTACAGATGCGTT CAAGAGACTCCGATTGTTGAGGTAAACGCGTT	4377
		AACCGCGTTACCTCAACAATGGAGTCTCTGAAACGCATCTGTAC CAATCATACGACGAG <u>A</u> GACTTGTCTGTGATTGCTACAAGAGGAA	4378
		CACTATCTAACAAACGCATCGGCTAACCGCT	4379
		GACAAGT <u>C</u> TCGTCGT	4380
		ACGACGAG <u>A</u> GACTTGTC	
10	Sulfonlurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAG	AGCGGATTAGCCGATGCGTTAGATAGTGTCTCTTAGCA ATCACAGGACAAGTC <u>C</u> AGCGTCGTATGATTGGTACAGATGCGTT CAAGAGACTCCGATTGTTGAGGTAAACGCGTT	4381
		AACCGCGTTACCTCAACAATGGAGTCTCTGAAACGCATCTGTAC CAATCATACGACG <u>T</u> GGACTTGTCTGTGATTGCTACAAGAGGAA	4382
		CACTATCTAACAAACGCATCGGCTAACCGCT	4383
		ACAAGT <u>C</u> AGCGTCGT	4384
		TACGACG <u>T</u> GGACTTGT	
15	Sulfonlurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAA	AGCGGATTAGCCGATGCGTTAGATAGTGTCTCTTAGCA ATCACAGGACAAGTC <u>C</u> AACGTCGTATGATTGGTACAGATGCGTT CAAGAGACTCCGATTGTTGAGGTAAACGCGTT	4385
		AACCGCGTTACCTCAACAATGGAGTCTCTGAAACGCATCTGTAC CAATCATACGACG <u>T</u> GGACTTGTCTGTGATTGCTACAAGAGGAA	4386
		CACTATCTAACAAACGCATCGGCTAACCGCT	4387
		ACAAGT <u>C</u> AACGTCGT	4388
		TACGACG <u>T</u> GGACTTGT	
20	Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAC	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCG <u>A</u> CGGTGGCACTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4389
		ATCTCTCAGTATTTAACCGGCCATCTCTCCGTATGACATCGT TGAAAGTGCCACC <u>G</u> TCGGGATCATCGGCAACACATGTTCTGGT GC GGACAAATCACATCCAACAGGTAAAGGT	4390
		GATCCC <u>G</u> AACGGTGGCA	4391
		TGCCACC <u>G</u> TCGGGATC	4392

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAT	GACCTTACCTGTTGGATGTGATTGTCGCCACCAAGAACATGTGT TGCCGATGATCCC <u>GAATGGTGGC</u> ACTTCAACGATGTCTAACCGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4393
		ATCTCTAGTATTAATCCGGCCATCTCCCTCCGTATGACATCGT TGAAAGTGCCACC <u>ATTCGGGAT</u> CATCGGCAACACATGTTCTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	4394
		GATCCC <u>GAATGGTGGC</u> A	4395
		TGCCACC <u>ATCGGGATC</u>	4396
10	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC	TCCCGCGCTCGCCGACCGCGCTGCTCGACTCCGTCGGATGGTCG CCATCACGGGCCAGGT <u>CTCCCCCGC</u> GATGATGGCACCGACGC CTTCCAGGAGACGCCATAGTCGAGGTACCCGCT	4397
		AGCGGGTGACCTCGACTATGGCGTCTCCTGGAAAGGCGTCGGT CCGATCATGCGGCGGG <u>AGAC</u> CTGGCCCGTATGGCGACCATCG GGACGGAGTCGAGCAGCGCTGGCGAGCGCGGA	4398
		GCCAGGT <u>CTCCCCGCC</u> G	4399
		GC <sup>G</sup> GGCGGG <u>AGAC</u> CTGGC	4400
		CCCGCGCTCGCCGACCGCGCTGCTCGACTCCGTCGGATGGTCG CATCACGGGCCAGGT <u>CCAAACGCC</u> GATGATGGCACCGACGCC TTCCAGGAGACGCCATAGTCGAGGTACCCGCT	4401
15	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA	GAGCGGGTGACCTCGACTATGGCGTCTCCTGGAAAGGCGTCGGT GCCGATCATGCGGCG <u>CTGG</u> ACCTGGCCCGTATGGCGACCATCG GGACGGAGTCGAGCAGCGCTGGCGAGCGCGG	4402
		CCAGGT <u>CCAAACGCC</u> GCA	4403
		TGCGGCG <u>CTGG</u> ACCTGG	4404
		CCCGCGCTCGCCGACCGCGCTGCTCGACTCCGTCGGATGGTCG CATCACGGGCCAGGT <u>CCAGCGCC</u> GATGATGGCACCGACGCC TTCCAGGAGACGCCATAGTCGAGGTACCCGCT	4405
		GAGCGGGTGACCTCGACTATGGCGTCTCCTGGAAAGGCGTCGGT GCCGATCATGCGGCG <u>CTGG</u> ACCTGGCCCGTATGGCGACCATCG GGGACGGAGTCGAGCAGCGCTGGCGAGCGCGG	4406
20	Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG	CCAGGT <u>CCAGCGCC</u> GCA	4407
		TGCGGCG <u>CTGG</u> ACCTGG	4408
		GGCCATACTGTTGGATATCATCGTCCCGACCAAGGAGCATGTGC TGCCTATGATCCC <u>AAATGGGGCG</u> CATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4409
		ATAGATTAATACACAGTCCTGCCATACCCATCCAGGATCATGTCCT TGAATGCGCCCC <u>CAATTGGGAT</u> CATAGGCAGCACATGCTCCTGGT GCGGGACGATGATCCAACAAGTATGCC	4410
		GATCCC <u>AAATGGGGCG</u> G	4411
25	Imidazolinone Resistance ALS <i>Oryza sativa</i> Ile627Asn ATT-AAT		
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG	CGCCCCCATTTGGGATC	4412
		TCCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCC TCCAGGAGACGCCATCGTCGAGGTACCCGCT	4413
		AGCGGGTGACCTCGACGATGGCGTCTCCTGGAAGGCGTCGG GCCAATCATGCGTCGCGACACCTGTCCCGTATGGCGACCATGG GGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	4414
		GACAGGTGTCGCGACGC	4415
		GCGTCGCGACACCTGTC	4416
		CCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGCAAGCGACGCATGATTGGCACCGACGCC CCAGGAGACGCCATCGTCGAGGTACCCGCTC	4417
10	Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG	GAGCGGGTGACCTCGACGATGGCGTCTCCTGGAAGGCGTCGG TGCCAATCATGCGTCGCTGCACCTGTCCCGTATGGCGACCATGG GGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	4418
		ACAGGTGCAAGCGACGC	4419
		TGCGTCGCTGCACCTGT	4420
		GGCCGTACCTCTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTAATGGTGGGCTTCAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4421
		TTAGATCAGTACACAGTCCTGCCATACCACATCCAGGATCATATCCT TGAAAGCCCCACCCATTAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4422
15	Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT	GATCCCTAATGGTGGGG	4423
		CCCCACCATAGGGATC	4424
		GGCCGTACCTCTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTAACGGTGGGCTTCAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4425
		TTAGATCAGTACACAGTCCTGCCATACCACATCCAGGATCATATCCT TGAAAGCCCCACCGTTAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4426
		GATCCCTAACGGTGGGG	4427
20	Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAC	CCCCACCGTTAGGGATC	4428
		GGCCGTACCTCTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTAACGGTGGGCTTCAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4425
		TTAGATCAGTACACAGTCCTGCCATACCACATCCAGGATCATATCCT TGAAAGCCCCACCGTTAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4426
		GATCCCTAACGGTGGGG	4427
25	Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Ser CCG-TCG	CCCCACCGTTAGGGATC	4428
		TCCCGCGCTCGCCGACGCCCTCTCGACTCCATCCCCATGGTGGC CATCACGGGGCAGGTCTCGCGCCGCATGATGGCACGGACGCC TTCCAGGAGACGCCATCGTCGAGGTACCCGCT	4429
		AGCGGGTGACCTCGACGATGGCGTCTCCTGGAAGGCGTCGG GCCGATCATGCGCGCGAGACCTGCCCCGTATGGCCACCATGG GGGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGGA	4430

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GGCAGGT <u>C</u> CGCGCCGC	4431
	GCGGCGCG <u>A</u> ACCTGCC	4432
5 Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Gln CCG-CAG	CCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGCC ATCACGGGGCAGGTC <u>C</u> ACGCCGCATGATGGCACGGACGCC	4433
	TCCAGGAGACGCCATCGTCGAGGTACCCGCT GAGCGGGTGACCTCGACGATGGCGTCTCTGGAAAGGCGTCCG	4434
	TGCCGATCATGCGGC <u>G</u> GGACCTGGCCCTGATGGCCACCATG	
	GGGATGGAGTCGAGGGAGGGCGTCGGCGAGCGCGG GCAGGT <u>C</u> ACGCCGC	4435
	TGCGGCG <u>G</u> GGACCTGC	4436
10 Imidazolinone Resistance ALS <i>Lolium multiflorum</i> Ser623Asn AGC-AAC	CTGGGCCATACTTGTGGATATCATCGTCCCTCACCAAGGAGCATG TGCTGCCTATGATCC <u>T</u> ACGGTGGTGCTTCAAGGACATTATCA	4437
	TGGAAAGGTGATGGCAGGATT <u>T</u> CGTATTAAAC GTTTAATACGAAATCTGCCATCACCTTCATGATAATGTCCTTGA	4438
	AAGCACCA <u>C</u> CGT <sup>T</sup> AGGGATCATAGGCAGCACATGTCCTGGTGA	
	GGGACGATGATATCCAACAAGTATGGCCAG GATCC <u>T</u> TA <u>C</u> GGTGGT	4439
	CACCACCG <u>T</u> AGGGATC	4440
15 Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Ser CCA-TCA	TCCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTGC CATCACGGGC <u>C</u> AGGT <u>T</u> CACGCCGCATGATGGCACGGACGCC	4441
	TCCAGGAGACGCCATAGTGGAGGTACCGC AGCGCGTGACCTCCACTATGGCGTCTCTGGAAACGCGTCCGT	4442
	CCGATCATGCGGC <u>T</u> GAGACCTGGCCCGTATGGCGACCATGG	
	GGATGGAGTCGAGGGAGAGCGTCGGCGAGCGCGGA GCCAGGT <u>C</u> ACGCCGC	4443
	GCGGCG <u>T</u> GAGACCTGGC	4444
20 Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Gln CCA-CAA	CCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTGC ATCACGGGC <u>C</u> AGGT <u>T</u> ACGCCGCATGATGGCACGGACGCC	4445
	CCAGGAGACGCCATAGTGGAGGTACCGC GAGCGCGTGACCTCCACTATGGCGTCTCTGGAAACGCGTCCGT	4446
	GCCGATCATGCGGC <u>T</u> GGACCTGGCCCGTATGGCGACCATGG	
	GGATGGAGTCGAGGGAGAGCGTCGGCGAGCGCGGA CCAGGT <u>C</u> ACGCCGC	4447
	TGC <u>G</u> GGCG <u>T</u> GGACCTGG	4448

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Imidazolinone Resistance ALS <i>Hordeum vulgare</i> Ser524Asn AGC-AAC	CCCAAGGGCCGTACCTGCTGGATATCATTGTCCCCCATCAGGAGC ACGTGCTGCCTATGATCCC <del>AA</del> ACGGTGGTGT <del>TT</del> CAAGGACATGA TCATGGAGGGTGTGGCAGGACCTCGTACTGA	4449
		TCAGTACGAGGTCTGCCATCACCC <del>CT</del> CATGATCATGTCCTGAA AGCACCACCG <del>TT</del> GGGATCATAGGCAGCACGTGCTCCTGATGCG GGACAA <del>T</del> ATGATCCAGCAGGTACGGCC <del>CT</del> GGG	4450
		GATCCC <del>AA</del> ACGGTGGT	4451
		CACCACCG <del>TT</del> GGGATC	4452
10	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTC <del>CT</del> CGTCGGATGATCGGTACCGATGCTTCC CAGGAAACTCCAATTGTTGAGGTAAACAAGGT	4453
		ACCTTGT <del>T</del> ACCTCAACAATTGGAG <del>TT</del> CCTGGAAAGCATCGGTAC CGATCATCCGACGAGAGACTTGACCAGTGTGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCAC	4454
		GTCAAGTC <del>CT</del> CGTCGG	4455
		CCGACGAGAGACTTGAC	4456
15	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTC <del>AA</del> CGTCGGATGATCGGTACCGATGCTTCC AGGAAACTCCAATTGTTGAGGTAAACAAGGT <del>C</del>	4457
		GACCTTGT <del>T</del> ACCTCAACAATTGGAG <del>TT</del> CCTGGAAAGCATCGGTAC CCGATCATCCGACG <del>CT</del> GGACTTGACCAGTGTGCCACGAGAGGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4458
		TCAAGTC <del>CC</del> ACGT <del>CG</del> GA	4459
		TCCGACG <del>CT</del> GGACTTGA	4460
20	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTC <del>AG</del> CGTCGGATGATCGGTACCGATGCTTCC AGGAAACTCCAATTGTTGAGGTAAACAAGGT <del>C</del>	4461
		GACCTTGT <del>T</del> ACCTCAACAATTGGAG <del>TT</del> CCTGGAAAGCATCGGTAC CCGATCATCCGACG <del>CT</del> GGACTTGACCAGTGTGCCACGAGAGGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4462
		TCAAGTC <del>CC</del> AGCGT <del>CG</del> GA	4463
		TCCGACG <del>CT</del> GGACTTGA	4464
25	Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT	GACCTTAC <del>TT</del> GGATGTGATTGTCCCCACATCAAGAACATGTCCT GCCTATGAT <del>CCC</del> <del>AA</del> TGGAGGCGCTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	4465
		TGAGGTCAATATTGTGTTCTCCATCACCC <del>CT</del> TGTGATCACATCTT TGAAAGCCCTCC <del>AA</del> TGGGGATCATAGGCAGGACATGTTCTGAT GTGGGACAATCACATCCAACAAGTAAGGT <del>C</del>	4466
		GATCCC <del>AA</del> ATGGAGGCG	4467

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CGCCTCCATTGGGGATC	4468
5 Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACITCTGACTCAGTCCCTTGTGCC TTACTGGGCAAGTT <u>CCCCGGCGT</u> TGATTGGTACTGATGCTTT AAGAGACTCCAATTGTTGAGGTAACTCGAT	4469
	ATCGAGTTACCTAACAAATTGGAGTCTCTGAAAAGCATCAGTAC AATCATACGCCGG <u>AA</u> ACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4470
	GGCAAGTT <u>CCCCGGCGT</u>	4471
	ACGCCGG <u>AA</u> ACTTGCC	4472
10 Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACITCTGACTCAGTCCCTTGTGCCA TTACTGGGCAAGTT <u>CAACGGCGT</u> TGATTGGTACTGATGCTTT AAGAGACTCCAATTGTTGAGGTAACTCGATC	4473
	GATCGAGTTACCTAACAAATTGGAGTCTCTGAAAAGCATCAGTAC CAATCATACGCCG <u>TTGA</u> ACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4474
	GCAAGTT <u>CAACGGCGT</u> A	4475
	TACGCCG <u>TTGA</u> ACTTGC	4476
15 Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACITCTGACTCAGTCCCTTGTGCCA TTACTGGGCAAGTT <u>CAGCGGGCGT</u> TGATTGGTACTGATGCTTT AAGAGACTCCAATTGTTGAGGTAACTCGATC	4477
	GATCGAGTTACCTAACAAATTGGAGTCTCTGAAAAGCATCAGTAC CAATCATACGCCG <u>CTGA</u> ACTTGCCCAGTAATGGCGACAAGAGGGA ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4478
	GCAAGTT <u>CAGCGGGCGT</u> A	4479
	TACGCCG <u>CTGA</u> ACTTGC	4480
25 Imidazolinone Resistance ALS <i>Amaranthus retroflexus</i> Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCAACATCAGGAGCATGTGC TGCCTATGATCCCTA <u>ACGGTGCCGCC</u> TTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4481
	ACCAACTAATAAGCCCTTCCATACCCTCTGTTATGGTGCCT TGAAGGCCGGCACCG <u>TTAGGGATCATAGGCAGCACATGCTCCTGA</u> TGTGGTACGATTACATCCAGCAGATA <u>CGGTC</u>	4482
	GATCCCTA <u>ACGGTGCCG</u>	4483
	CGGCACCG <u>TTAGGGATC</u>	4484

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Ser CCA-TCA	AGCGGCCTCGCTGACCGCCTACTGGATAGCGTCCCCATTGTTGC TATAACAGGTCAAGT <u>G</u> CACGTAGGATGATAGGTACTGATGCTTT CAGGAAACTCCTATTGTTGAGGTAACAGAT	4485
		ATCTAGTTACCTCAACAATAGGAGTTCTGAAAAGCATCAGTACC TATCATCCTACGT <u>G</u> ACATTGACCTGTTAGCAACAATGGGAC GCTATCCAGTAGCGCGTCAGCGAGGCCGCT	4486
		GTCAAGT <u>G</u> T <u>C</u> ACGTAGG	4487
		CCTACGT <u>G</u> ACATTGAC	4488
10	Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Gln CCA-CAA	GCAGGCCTCGCTGACCGCCTACTGGATAGCGTCCCCATTGTTGCT ATAACAGGTCAAGT <u>G</u> CA <u>A</u> CGTAGGATGATAGGTACTGATGCTTT CAGGAAACTCCTATTGTTGAGGTAACAGATC	4489
		GATCTAGTTACCTCAACAATAGGAGTTCTGAAAAGCATCAGTAC CTATCATCCTACGT <u>G</u> CACTTGACCTGTTAGCAACAATGGGAC CGCTATCCAGTAGCGCGTCAGCGAGGCCGCT	4490
		TCAAGT <u>G</u> CA <u>A</u> CGTAGG	4491
		TCCTACGT <u>G</u> CACTTGAC	4492
15	Imidazolinone Resistance ALS 1 <i>Nicotiana tabacum</i> Ser650Asn AGT-AAT	GGCCATACTTGGATGTGATTGTACCTCATCAGGAACATGTTTT ACCTATGATTCCCA <u>A</u> GGCGGAGCTTCAAAGATGTGATCACAGA GGGTGACGGGAGAA <u>G</u> TTCTATTGAGTTG	4493
		CAAAC <sup>T</sup> CAATAGGA <u>A</u> CTTCTCCCGTACCCCTGTGATCACATCTT TGAAAGCTCCGCCA <u>T</u> GGGAATCATAGGAAAACATGTTCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4494
		GATTCCCA <u>A</u> GGCGGAG	4495
		CTCCGCC <u>A</u> GGGAATC	4496
20	Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Ser CCA-TCA	AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC TATAACC <u>G</u> GTCAAGT <u>G</u> CACGTAGGATGATCGGTACTGATGCTTT CAGGAAACTCCGATTGTTGAGGTAACAGAT	4497
		ATCTAGTTACCTCAACAATCGGAGTTCTGAAAAGCATCAGTACC GATCATCCTACGT <u>G</u> ACATTGACCGGTTAGCAACAATGGGAC GCTATCCAGTAGGGCGTCCCGCAGGCCACT	4498
		GTCAAGT <u>G</u> T <u>C</u> ACGTAGG	4499
		CCTACGT <u>G</u> ACATTGAC	4500
25	Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Gln CCA-CAA	GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT ATAACC <u>G</u> GTCAAGT <u>G</u> CA <u>A</u> CGTAGGATGATCGGTACTGATGCTTT CAGGAAACTCCGATTGTTGAGGTAACAGATC	4501
		GATCTAGTTACCTCAACAATCGGAGTTCTGAAAAGCATCAGTAC CGATCATCCTACGT <u>G</u> CACTTGACCTGACCGGTTAGCAACAATGGGAC CGCTATCCAGTAGGGCGTCCCGCAGGCCACT	4502
		TCAAGT <u>G</u> CA <u>A</u> CGTAGG	4503

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		TCCTACGTTGCACTTGA	4504
5	Imidazolinone Resistance ALS 2 <i>Nicotiana tabacum</i> Ser647Asn AGT-AAT	GGCCATACTTGTGGATGTGATTGACCTCATCAGGAACATGTTCTACCTATGATCCCA <u>ATGGCGGGGCTTCAAAGATGTGATCACAGA</u> GGGTGACGGGAGAAGTCCTATTGACTTTG	4505
		CAAAGTCAATAGGAACCTCTCCCGTCACCCCTGTGATCACATCTT TGAAAGCCCCGCCATTGGGAATCATAGGTAGAACATGTTCTGATGAGGTACAATCACATCCAACAAAGTATGGCC	4506
		GATTCCCA <u>ATGGCGGGG</u>	4507
		CCCCGCCATTGGGAATC	4508
10	Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Ser CCC-TCC	AGTGGTCTTGCTGATGCTTTATTAGACAGTGTCCAATGGTTGCTA TTACTGGTCAAGTT <u>CCAGGAGAACATGATTGAAACAGATGCGTTCA</u> AGAAACCCCTATTGTTGAGGTAAACACGTT	4509
		AACGTGTTACCTCAACAATAGGGTTCTGAAACGCATCTGTTCC AATCATTCTCCTGGAAACTGACCAGTAATAGCAACCATTGGAACA CTGTCTAATAAAGCATCAGCAAGACCACT	4510
		GTCAAGTT <u>CCAGGAGA</u>	4511
		TCTCCTGGAAACTTGAC	4512
		GTGGTCTTGCTGATGCTTTATTAGACAGTGTCCAATGGTTGCTAT TACTGGTCAAGTT <u>CAAGGAGAACATGATTGAAACAGATGCGTTCA</u> AGAAACCCCTATTGTTGAGGTAAACACGTT	4513
15	Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAA	GAACGTGTTACCTCAACAATAGGGTTCTGAAACGCATCTGTTCC CAATCATTCTCCT <u>TGAACTTGACCAGTAATAGCAACCATTGGAAC</u> ACTGTCTAATAAAGCATCAGCAAGACCACT	4514
		TCAAGTT <u>CAAGGAGAA</u>	4515
		TTCTCCT <u>TGAACTTGA</u>	4516
		GTGGTCTTGCTGATGCTTTATTAGACAGTGTCCAATGGTTGCTAT TACTGGTCAAGTT <u>CAAGGAGAACATGATTGAAACAGATGCGTTCA</u> AGAAACCCCTATTGTTGAGGTAAACACGTT	4517
		GAACGTGTTACCTCAACAATAGGGTTCTGAAACGCATCTGTTCC CAATCATTCTCCT <u>TGAACTTGACCAGTAATAGCAACCATTGGAAC</u> ACTGTCTAATAAAGCATCAGCAAGACCACT	4518
20	Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAG	TCAAGTT <u>CAAGGAGAA</u>	4519
		TTCTCCT <u>TGAACTTGA</u>	4520
		GGGCCTTACTTGTGGATGTGATCGTGCCCCATCAAGAACATGTG TTGCCCATGATCCC <u>GAATGGTGAGGTTCATGGATGTGATCACCGAAGGCGACGGCAGAACATGAAATTGAGCTT</u>	4521
		AAGCTCAATATTCTATTCTGCCCGCCTCGGTGATCACATCCAT GAAACCTCCACCA <u>ATTGGGATCATGGGCAACACATGTTCTGATGGGCACGATCACATCCAACAAAGTAAGGCC</u>	4522
25	Imidazolinone Resistance ALS <i>Xanthium</i> spp. Ala631Asn GCT-AAT		
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Ser CCG-TCG	TGATCCCG <u>A</u> ATGGTGGA	4523
		TCCACCA <u>T</u> CGGGATCA	4524
		TCCGGGTTGCTGATGCTTGCTCGATTCCGTCCACTGGTGGCG ATCACGGGGCAGGTG <u>T</u> CGCGCCGAATGATTGGGACGGATGCTT TCAGGAGACTCCTATTGTTGAGGTAAACACGGT	4525
		ACCGTGTACCTCAACAATAGGAGTCTCTGAAAAGCATCCGTCC CAATCATTGCGCCG <u>G</u> <u>A</u> CACCTGCCCCGTGATGCCACCAAGTGG ACGGAATCGAGCAAAGCATCAGCAAACCCGG	4526
		GGCAGGTG <u>T</u> CGCGCGA	4527
		TCGCCGCG <u>G</u> <u>A</u> CACCTGCC	4528
	Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Gln CCG-CAG	CCGGGTTGCTGATGCTTGCTCGATTCCGTCCACTGGTGGCGA TCACGGGGCAGGTG <u>C</u> <u>A</u> GC <u>G</u> CGCAATGATTGGGACGGATGCTTT CAGGAGACTCCTATTGTTGAGGTAAACACGGTC	4529
		GACCGTGTACCTCAACAATAGGAGTCTCTGAAAAGCATCCGTCC CCAATCATTGCGCCG <u>T</u> GCACCTGCCCCGTGATGCCACCAAGTGG AACGGAATCGAGCAAAGCATCAGCAAACCCGG	4530
		GCAGGTG <u>C</u> <u>A</u> GC <u>G</u> CGAA	4531
		TTCGCCG <u>G</u> <u>T</u> GCACCTGC	4532
		GACCTTACCTGCTGATGTGATTGATCCTCATCAGGAGCATGTGC TGCCTATGATTCT <u>A</u> ATGGTG <u>C</u> <u>A</u> GCCTTCAAGGATATCATTAAACGA AGGTGATGGAAGAACAGTTATTGATGTT	4533
10	Imidazolinone Resistance ALS <i>Bassia scoparia</i> Ser649Asn AGT-AAT	GAACATCAATAACTTGTCTTCATCACCTCGTTAATGATATCCTT GAAGGCTGCACCA <u>T</u> AGGAATCATAGGCAGCAGCATGCTCCTGATG AGGTACAATCACATCAAGCAGGTAAGGTC	4534
		GATTCT <u>A</u> ATGGTGCAG	4535
		CTGCACCA <u>T</u> AGGAATC	4536
		AGCGGGTTAGCAGACGCGATGCTTGACAGTGTCTCTTGT <u>C</u> <u>G</u> CATTACAGGACAGGT <u>C</u> <u>T</u> CGCCGGATGATCGGTACTGACGCC CCAAGAGAACCAATCGTTGAGGTAAACGAGGT	4537
		ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAAGGCGTCAGTAC CGATCATCCGGCGAG <u>A</u> GACCTGTCCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCGCT	4538
15	Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Ser CCT-TCT	GACAGGT <u>C</u> <u>T</u> CGCCGG	4539
		CCGGCGAG <u>A</u> GACCTGTC	4540

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAA	GCGGGTTAGCAGACCGATGCTGACAGTGTCCCTTGTGCC ATTACAGGACAGGTCAACGCCGGATGATCGGTACTGACGCC CCAAGAGACACCAATCGTTGAGGTAAACGAGGT	4541
		GACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCAGTA CCGATCATCCGGCGTGGACCTGTCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCGC	4542
		ACAGGTCCAACGCCGA	4543
		TCCGGCGTGGACCTGT	4544
		GCAGGGTTAGCAGACCGATGCTGACAGTGTCCCTTGTGCC ATTACAGGACAGGTCCAGGCCGGATGATCGGTACTGACGCC CCAAGAGACACCAATCGTTGAGGTAAACGAGGT	4545
10	Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAG	GACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCAGTA CCGATCATCCGGCGTGGACCTGTCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCGC	4546
		ACAGGTCCAGGCCGA	4547
		TCCGGCGTGGACCTGT	4548
		GACCACCTGGATGTGATATGTCGGCACCAAGAACATGTG TACCGATGATCCAAATGGTGGCACTTCAAAGATGTAATAACAGA AGGGGGATGGTCGCACTAAGTACTGAGAGAT	4549
		ATCTCTCAGTACTAGTGCACCATCCCCCTCTGTTATTACATCTT TGAAAGTGCCACCAATTGGGATCATCGGTAAACACATGTTCTGGT GCGGACATATCACATCCAACAGGTATGGTC	4550
15	Imidazolinone Resistance ALS 1 <i>Brassica napus</i> Ser638Asn AGT-AAT	GATCCCAAATGGTGGCA	4551
		TGCCACCAATTGGGATC	4552
		CAGCGGGTTAGCAGACCGATGCTGACAGTGTCCCTTGTGCG CCATTACAGGACAGGTCCCTCGCCGGATGATCGGTACTGACGCC TTCCAAGAGACACCAATCGTTGAGGTAAACGAGG	4553
		CCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCAGTA GATCATCCGGCGAGGAACCTGTCTGTAATGGCGACAAGAGGAA CACTGTCAAGCATCGCGTCTGCTAACCGCTG	4554
		GGACAGGTCCCTCGCCG	4555
20	Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Ser CCC-TCC	CGGCGAGGAAACCTGTCC	4556
		AGCGGGTTAGCAGACCGATGCTGACAGTGTCCCTTGTGCG CATTACAGGACAGGTCACTCGCCGGATGATCGGTACTGACGCC TCCAAGAGACACCAATCGTTGAGGTAAACGAGGT	4557
		ACCTCGTTACCTCAACGATTGGTGTCTTGGAAAGGCAGTA CGATCATCCGGCGAGGTGACCTGTCTGTAATGGCGACAAGAGGAA ACACTGTCAAGCATCGCGTCTGCTAACCGCT	4558
		GACAGGTCACTCGCCGG	4559
25	Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Gln CCC-CAG		
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		CCGGCGAG <u>T</u> GACCTGTC	4560
5	Imidazolinone Resistance ALS 2 <i>Brassica napus</i> Ser582Asn AGT-AAT	GACCATAACCTGTTGGATGTGATATGTCGGCACCAAGAACATGTGT TACCGATGAT <u>CCCAATGGTGGCA</u> TTCAAAGATGTAATAACAGA AGGGGATGGTCGCACTAAGTACTGAGAGAT	4561
		ATCTCTCAGTACTTAGTGC <u>GACCATCCCCCTCGT</u> TATTACATCTT TGAAAGTGC <u>CAACATTGGGAT</u> CATCGGTAA <u>ACACATGTTCTGGT</u> GCGGACATATCACATCCAACAGGTATGGTC	4562
		GAT <u>CCCAATGGTGGCA</u>	4563
		TGCCACCA <u>TTGGGATC</u>	4564
10	Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Ser CCT-TCT	AGCGGGTTAGCCGACGGCATGCTTGACAGTGTCCCTCGTCGCC CATCACAGGACAGGT <u>CTCGCCGGATGATCGGTACTGACGCGT</u> TCCAAGAGACGCCAATCGTTGAGGTAA <u>CGAGGT</u>	4565
		ACCTCGTTACCTCAACGATTGGCGTCTCTGGAAC <u>CGCGTCAGTAC</u> CGATCATCCGGCGAGAGAC <u>CTGTCCTGT</u> GATGGCGACGAGAGGA ACACTGTCAAGCATCGCGT <u>CGGCTAACCCGCT</u>	4566
		GACAGGT <u>CTCGCCGG</u>	4567
		CCGGCGAG <u>AGACCTGTC</u>	4568
		GC <u>GGGGTTAGCCGACGGCATGCTTGACAGTGTCCCTCGTCGCC</u> ATCACAGGACAGGT <u>CCAACGCCGGATGATCGGTACTGACGCGT</u> CCAAGAGACGCCAATCGTTGAGGTAA <u>CGAGGT</u>	4569
15	Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAA	GACCTCGTTACCTCAACGATTGGCGTCTCTGGAAC <u>CGCGTCAGTAC</u> CCGATCATCCGGCG <u>TTGGACCTGT</u> CCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGT <u>CGGCTAACCCGCT</u>	4570
		ACAGGT <u>CCAACGCCGG</u>	4571
		T <u>CCGGCGT</u> GGACCTGT	4572
		GC <u>GGGGTTAGCCGACGGCATGCTTGACAGTGTCCCTCGTCGCC</u> ATCACAGGACAGGT <u>CCAGCGCCGGATGATCGGTACTGACGCGT</u> CCAAGAGACGCCAATCGTTGAGGTAA <u>CGAGGT</u>	4573
		GACCTCGTTACCTCAACGATTGGCGTCTCTGGAAC <u>CGCGTCAGTAC</u> CCGATCATCCGGCG <u>CTGGACCTGT</u> CCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGT <u>CGGCTAACCCGCT</u>	4574
20	Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAG	ACAGGT <u>CCAAGCGCCGG</u>	4575
		T <u>CCGGCGT</u> GGACCTGT	4576
		GC <u>GGGGTTAGCCGACGGCATGCTTGACAGTGTCCCTCGTCGCC</u> ATCACAGGACAGGT <u>CCAGCGCCGGATGATCGGTACTGACGCGT</u> CCAAGAGACGCCAATCGTTGAGGTAA <u>CGAGGT</u>	4577
		GACCTCGTTACCTCAACGATTGGCGTCTCTGGAAC <u>CGCGTCAGTAC</u> CCGATCATCCGGCG <u>CTGGACCTGT</u> CCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGT <u>CGGCTAACCCGCT</u>	4578
		ACAGGT <u>CCAGCGCCGG</u>	4579
25	Imidazolinone Resistance ALS 3 <i>Brassica napus</i> Ser635Asn AGT-AAT	GACCGTACCTGTTGGATGT <u>CATCTGTCGGCACCAAGAACATGTGT</u> TACCGATGAT <u>CCCAATGGTGGCA</u> TTCAAAGATGTAATAACCG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	4577
		ATCTCTCAGTACTTAGTGC <u>GACCATCCCCCTCGT</u> TATTACATCTT TGAAAGTGC <u>CAACATTGGGAT</u> CATCGGTAA <u>ACACATGTTCTGGT</u> GCGGACAGATGAC <u>ATCCAACAGGTACGGTC</u>	4578

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GATCCCAA <u>A</u> GGTGGCA	4579
	TGCCACCA <u>T</u> GGGATC	4580
5 Sulfonylurea Resistance ALS Oryza sativa Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCGGATGGTCG CCATCACGGGCCAGGT <u>C</u> CCCGCCGATGATGGCACCGACGC CTTCCAGGAGACGCCATAGTCGAGGTACCCGCT	4581
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT CCGATCATGCGCGGGAGACCTGGCCCGTATGGCACCACG GGACGGAGTCGAGCAGCGCTGGCGAGCGCGGA	4582
	GCCAGGT <u>C</u> CCCGCCGC	4583
	GCGGCGGG <u>A</u> GACCTGGC	4584
	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCGGATGGTCG CATCACGGGCCAGGT <u>C</u> ACGCCGATGATGGCACCGACGC TTCCAGGAGACGCCATAGTCGAGGTACCCGCTC	4585
10 Sulfonylurea Resistance ALS Oryza sativa Pro171Gln CCC-CAA	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGCG <u>T</u> GGACCTGGCCCGTATGGCACCACG GGACGGAGTCGAGCAGCGCTGGCGAGCGCGG	4586
	CCAGGT <u>C</u> ACGCCGA	4587
	TGCGGC <u>G</u> GGACCTGG	4588
	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCGGATGGTCG CATCACGGGCCAGGT <u>C</u> AGGCCGATGATGGCACCGACGC TTCCAGGAGACGCCATAGTCGAGGTACCCGCTC	4589
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGCG <u>C</u> GGACCTGGCCCGTATGGCACCAC GGGACGGAGTCGAGCAGCGCTGGCGAGCGCGG	4590
15 Sulfonylurea Resistance ALS Oryza sativa Pro171Gln CCC-CAG	CCAGGT <u>C</u> AGGCCGA	4591
	TGCGGC <u>G</u> GGACCTGG	4592
	GGCCATACT <u>T</u> GGATATCATCGTCCCGACCAAGGAGCATGTG TGCCTATGATCCAA <u>A</u> GGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4593
	ATAGATTAATAACACAGTCTGCCATACCCATCCAGGATCATGTCCT TGAATGCGCCCC <u>C</u> TTGGGATCATAGGCAGCACATGCTCCTGGT GGGGACGATGATCCAACAAGTATGGCC	4594
	GATCCCAA <u>A</u> GGGGCG CGCCCC <u>C</u> TTGGGATC	4595 4596
20 Imidazolinone Resistance ALS Oryza sativa Ser627Asn AGT-AAT		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG	TC TCGCGCTCGCAGACGCGTTGCTCGACTCCGCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCT TTCAGGAGACGCCATCGTCGAGGTACCCGCT	4597
		AGC GGGGTGACCTCGACGATGGCGTCTCTGAAAGGCGTCGGT CCAATCATGCGTCGCGACACCTGTCCCGTATGGCGACCATGGG GACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA	4598
		GACAGGTGTCGCGACGC	4599
		GCGTCGCGACACCTGTC	4600
10	Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG	CT TCGCGCTCGCAGACGCGTTGCTCGACTCCGCCCCATGGTCGCC ATCACGGGACAGGTGCAAGCGACGCATGATTGGCACCGACGCCTT TCAGGAGACGCCATCGTCGAGGTACCCGCTC	4601
		GAGC GGGGTGACCTCGACGATGGCGTCTCTGAAAGGCGTCGGT GCCAATCATGCGTCGCTGCACCTGTCCCGTATGGCGACCATGG GGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG	4602
		ACAGGTGCAAGCGACGCA	4603
		TGCGTCGCTGCACCTGT	4604
15	Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT	GGCCGTACCTCTGGATATAATCGTCCCGCACCAAGGAGCATGTGT TGCCTATGATCCCTAATGGTGGGGTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTATTGATCCGT	4605
		ACGGATCAATACACAGTCTGCCATCACCATCCAGGATCATATCC TTGAAAGCCCCACCAATTAGGGATCATAGGCAACACATGCTCCTGG TGCGGGACGATTATATCCAAGAGGTACGGC	4606
		GATCCCTAATGGTGGGG	4607
		CCCCACCAATTAGGGATC	4608
20	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTCTCGTCGGATGATCGGTACCGATGCTTCC CAGGAAACTCCAATTGTTGAGGTAACAAGGT	4609
		ACCTTGTTACCTCAACAATTGGAGTTCTGGAAAGCATCGGTAC CGATCATCCGACGAGAGACTTGACCAGTGATGCCACGAGAGGG ATACTATCGAGCATTGATCAGCGAGACCACT	4610
		GTCAAGTCTCTCGTCGG	4611
		CCGACGAGAGACTTGAC	4612
25	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCCAACGTGGATGATCGGTACCGATGCTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGT	4613
		GACCTTGTTACCTCAACAATTGGAGTTCTGGAAAGCATCGGTAC CCGATCATCCGACGTTGGACTTGACCAGTGATGCCACGAGAGGG GATACTATCGAGCATTGATCAGCGAGACCACT	4614
		TCAAGTCCAACGTGGAA	4615

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		TCCGACG <u>T</u> GGACTTGA	4616
5	Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAG <u>T</u> CC <u>A</u> CGCGTCCGATGATCGGTACCGATGCTTCC AGGAAACTCAATTGTTGAGGTACAAGGTC	4617
		GACCTTGTACCTCAACAATTGGAGTTCTGGAAAGCATCGTA CCGATCATCCGACG <u>T</u> GGACTTGACCAGTATGCCACGAGAGG GATACTATCGAGCATTGATCAGCGAGACCAC	4618
		TCAAGTCC <u>A</u> CGCGTCCGA	4619
		TCCGACG <u>C</u> GGACTTGA	4620
10	Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT	GACCTTACTTGTGGATGTGATTGTCCCACATCAAGAACATGTCCT GCCTATGATCCCC <u>A</u> TGGAGGGGCTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	4621
		TGAGGTCAATATTGTTCTCCATCACCCCTGTGATCACATCTT TGAAAGCCCCTCC <u>A</u> TGGGGATCATAGGCAGGACATGTTCTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	4622
		GATCCCC <u>A</u> TGGAGGGG	4623
		CCCCTCC <u>A</u> TGGGGATC	4624
		CTGGTCTTGCTGATGCACTTCTGACTCAGTCCCTCTTGTGCC TTACTGGGCAAG <u>T</u> CCCGGGTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGAT	4625
15	Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Ser CCC-TCC	ATCGAGTTACCTCAACAATTGGAGTCTTGA <u>AA</u> AGCATCAGTACC AATCATACGCCGG <u>A</u> ACTTGGCCAGTAATGGCGACAAGAGGG CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4626
		GGCAAGT <u>T</u> CCCGGGT	4627
		ACGCCGG <u>A</u> ACTTGC	4628
		CTGGTCTTGCTGATGCACTTCTGACTCAGTCCCTCTTGTGCC TTACTGGGCAAG <u>T</u> CA <u>A</u> CGGGTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGATC	4629
		GATCGAGTTACCTCAACAATTGGAGTCTTGA <u>AA</u> AGCATCAGTAC CAATCATACGCCG <u>T</u> GA <u>A</u> CTTGGCCAGTAATGGCGACAAGAGGG CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4630
20	Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAA	GCAAGT <u>T</u> CA <u>A</u> CGGGTAA <u>A</u> CTTGC	4631
		TACGCCG <u>T</u> GA <u>A</u> CTTGC	4632
		CTGGTCTTGCTGATGCACTTCTGACTCAGTCCCTCTTGTGCC TTACTGGGCAAG <u>T</u> CA <u>A</u> CGGGTATGATTGGTACTGATGCTTTC AAGAGACTCCAATTGTTGAGGTAACTCGATC	4633
		GATCGAGTTACCTCAACAATTGGAGTCTTGA <u>AA</u> AGCATCAGTAC CAATCATACGCCG <u>T</u> GA <u>A</u> CTTGGCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4634
25	Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAG		
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Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCAAGTTC <u>A</u> GC <u>G</u> CGTA	4635
	TACGCC <u>G</u> CTGA <u>A</u> TTGC	4636
Imidazolinone Resistance ALS <i>Amaranthus powellii</i> Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCA <u>C</u> ATCAGGAGC <u>A</u> TGTGC TGCCTATGATCC <u>C</u> TA <u>A</u> CGGTGCC <u>G</u> CTTC <u>A</u> AGGACACC <u>A</u> ACAG AGGGT <u>G</u> ATGGA <u>A</u> GAAGGG <u>C</u> TTATTAGTTGGT ACCAACTAATAAGCC <u>C</u> TT <u>C</u> TC <u>C</u> AT <u>C</u> ACC <u>C</u> CT <u>T</u> G <u>T</u> ATGGTGT <u>C</u> CT TGAAGGCGG <u>C</u> ACC <u>G</u> TT <u>AG</u> GG <u>A</u> T <u>C</u> AT <u>AG</u> GC <u>A</u> CG <u>A</u> AT <u>G</u> CT <u>C</u> CTGA TGTGGT <u>A</u> CG <u>T</u> ATT <u>A</u> CC <u>A</u> GC <u>A</u> G <u>T</u> ACGGTC GATCC <u>C</u> TA <u>A</u> CGGTGCC <u>G</u> CGGCACCG <u>T</u> TT <u>AG</u> GG <u>A</u> T <u>C</u>	4637 4638 4639 4640

**Table 12**  
**Genome-Altering Oligos Conferring Porphyric Herbicide Resistance**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Porphyric Herbicide Resistant PPO <i>Arabidopsis thaliana</i> Val365Met GTT-ATG	TCTTGCGCCCTTTCTGAATCTGCTGCAAATGCACTCTCAAAACT ATATTACCCACCAAT <u>GGCAGCAGTATCTATCTCGTACCGAAAGA</u> AGCAATCCGAACAGAATGTTGATAGATGG	4641
		CCATCTATCAAACATTCTGTTGGATTGCTTCTTGGGTACGAGA TAGATACTGCTGCCATTGGTGGTAATATAGTTTGAGAGTCATT TGCAGCAGATTAGAAAGAGGGCGCAAGA	4642
		CCCACCA <u>ATGGCAGCAG</u>	4643
		CTGCTGCCATTGGTGGG	4644
10	Porphyric Herbicide Resistant PPO <i>Nicotiana tabacum</i> Val376Met GTT-ATG	TATTACGTCCCTTTGGTGGCGCAGCAGATGCACTTCAAATT CTACTATCCCCA <u>ATGGGAGCAGTCACAATTTCATATCCTCAAGAA</u> GCTATTCTGATGAGCGTCTGGTTGATGG	4645
		CCATCAACCAGACGCTCATCAGAATAGCTTCTGAGGATATGAA ATTGTGACTGCTCC <u>ATTGGGGATAGTAGAAATTGAAAGTGCA</u> TCTGCTGCGGCAACCGAAAGAGGGACGTAATA	4646
		TCCCCC <u>ATGGGAGCAG</u>	4647
		CTGCTCC <u>ATTGGGGGA</u>	4648
		TGTTGCGTCCGCTTCGTTGGGTGCAGCAGATGCATTGTC TTTATTATCCTCCG <u>ATGGCAGCTGTATCAATTTCATATCCAAAAGA</u> CGCAATTCTGTGCTGACCGGCTGATTGATGG	4649
15	Porphyric Herbicide Resistant PPO <i>Cichorium intybus</i> Val383Met GTT-ATG	CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTGGATATGAA ATTGATACAGCTGCC <u>ATCGGAGGATAATAAAATTGACAATGCAT</u> CTGCTGCACCAACGAAAGCGGACGCAACA	4650
		TCCTCCG <u>ATGGCAGCTG</u>	4651
		CAGCTGCC <u>ATCGGAGGAA</u>	4652
		TCCTTCGTCCACTTCAGATGTCGCCGAGAATCTCTTCAAATT TCATTATCCACCA <u>ATGGCAGCTGTGTCAC</u> TTCTATCCTAAAGAA GCAATTAGATCAGAGTGCCTGATTGACGG	4653
		CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTAGGATAGGAA GTGACACAGCTGCC <u>ATTGGTGGATAATGAAATTGAAAGAGATT</u> TGCAGGACATCTGAAAGTGGACGAAAGGA	4654
20	Porphyric Herbicide Resistant PPO <i>Spinacia oleracea</i> Val390Met GTT-ATG	TCCACCA <u>ATGGCAGCTG</u>	4655
		CAGCTGCC <u>ATTGGTGGAA</u>	4656

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Porphyric Herbicide Resistant PPO <i>Zea mays</i> Val363Met GTT-ATG	TTTGCGTCCACTTCAAGCGATGCTGCAGATGCTCTATCAAGATT CTATTATCCACCGA <u>TGG</u> CTGCTGTAAGTGGTATCCAAAGGAA GCAATTAGAAAAGAATGCTTAATTGATGG	4657
		CCATCAATTAAAGCATTCTTCTAATTGCTTCCTTGGATACGAAAC AGTTACAGCAGCC <u>ATCGG</u> TGGATAATAGAATCTTGATAGAGGCATC TGCAGCATCGCTTGAAGTGGACGAAAA	4658
		TCCACCGA <u>TGG</u> CTGCTG	4659
		CAGCAGCC <u>ATCGG</u> TGGA	4660
10	Porphyric Herbicide Resistant PPO <i>Oryza sativa</i> Val364Met GTT-ATG	TCTTGCGCCACTTCAAGTGTGAGCAGATGCTCTGTCATATT CTATTATCCACCA <u>ATGG</u> CTGCTGTAAGTGGTATCCAAAGAA GCAATTAGAAAAGAATGCTTAATTGACGG	4661
		CCGTCAATTAAAGCATTCTTCTAATTGCTTCCTTGGATATGAAAC AGTTACAGCAGCC <u>ATGG</u> TGGATAATAGAATATTGACAGAGGCATCT GCTGCATCACTGAAAGTGGCCGCAAGA	4662
		TCCACCA <u>ATGG</u> CTGCTG	4663
		CAGCAGCC <u>ATGG</u> TGGA	4664
15	Porphyric Herbicide Resistant PPO <i>Chlamydomonas reinhardtii</i> Val389Met GTG-ATG	CTGGTCAAGGAGCAGGCAGCCGCCGCCGCCGAGGCCCTGGCT CCTTCGACTACCCGCC <u>ATGG</u> CGCCGTGACGCTGTCGACCCG CTGAGCGCCGTGCGGGAGGAGCGCAAGGCCCTCGG	4665
		CCGAGGCCTTGCCTCCCGCACGGCCTCAGCGGGTACGA CAGCGTCACGGGCC <u>ATCGG</u> GGGTAGTCGAAGGAGGCCAGG GCCTCGGCGGGCGGCCCTGCTCCTGACCAG	4666
		ACCCGCC <u>ATGG</u> CGCC	4667
		GGCGCCC <u>ATCGG</u> GGGT	4668

20

Table 13  
Genome-Altering Oligos Conferring Triazine Resistance

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
25	Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTACGGTTATTTGGCCGATTGAT TTCCAATATGCT <u>AC</u> TTCAACAATTCTGTTCTTACATTCTCTT AGCGGCTGGCCGGTAGTAGGTATTG	4669
		CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGAAAGAA CGAGAATTGTTGAAG <u>AT</u> GCATATTGAAATCAATCGGCCAAAT AACCCTGAGCAGCTACAATGTTGAAGTT	4670

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT	ATATGCT <u>ACT</u> TTCAACA	4671
		TGTTGAA <u>AGT</u> AGCATAT	4672
		AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACTCTCGTTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4673
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAA <u>AGT</u> AGCATATTGGAAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATTTAAGTTT	4674
		ATATGCT <u>ACT</u> TTCAACA	4675
		TGTTGAA <u>AGT</u> AGCATAT	4676
10	Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACTCTCGCTCTTACATTCTCTC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4677
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGAATGTAAAGAG CGAGAGTTGTTAA <u>AGT</u> AGCATATTGGAAAGATCAATCGGCCAAAAAT AACCATGAGCGGCTACGATATTATAAGTTT	4678
		ATATGCT <u>ACT</u> TTCAACA	4679
		TGTTAA <u>AGT</u> AGCATAT	4680
		AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACTCTCGTTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4681
15	Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGAATGTAAAGAG CGAGAGTTGTTGAA <u>AGT</u> AGCATATTGGAAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4682
		ATATGCT <u>ACT</u> TTCAACA	4683
		TGTTGAA <u>AGT</u> AGCATAT	4684
		AAACTTATAATATCGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACTCTCGTTCGTTACATTCTCTC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4685
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGAATGTAAAGAA CGAGAATTGTTGAA <u>AGT</u> AGCATATTGGAAAGATCAATCGGCCAAAAAT AACCATGAGCAGCTACGATATTATAAGTTT	4686
20	Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT	ATATGCT <u>ACT</u> TTCAACA	4687
		TGTTGAA <u>AGT</u> AGCATAT	4688
		AAACCTTATAATTGAGCAGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>ACT</u> TTCAACAACTCTCGTTCGTTACATTCTCTC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4689
		CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGAATGTAAAGAA CGAGAGTTGTTGAA <u>AGT</u> AGCATATTGGAAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATTATAAGTTT	4690
		ATATGCT <u>ACT</u> TTCAACA	4691
25	Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		TGTTGAAAGTAGCATAT	4692
5	Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCAACTTCAACAATTCTCGTTCTTACATTCTTCT TAGCTGCTGGCCTGTAGTAGGTATTG	4693
		CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAT AACCATGAGCAGCTACAATATTATAGGTT	4694
		ATATGCAAC <del>TTT</del> CAACA	4695
		TGTTGAAAGTAGCATAT	4696
		AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCT <del>A</del> TTCAACAATTCTCGTTCTTACATTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTG	4697
10	Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAT AACCCTGAGCAGCTACAATGTTGAAGTT	4698
		ATATGCT <del>A</del> TTTCAACA	4699
		TGTTGAAAGTAGCATAT	4700
		AAACTTATAATATTGTGGCCGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCTACTTTAACAACTCTCGTTCTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTG	4701
		CAAATCCCTACTACAGGCCAAGCAGCCAGAAAGAAGTGTAAAGAA CGAGAGTTGTTAAAGTAGCATATTGGAAGATTAATCGGCCAAAT AACCATGAGCGGCCACAATATTATAAGTT	4702
15	Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	ATATGCT <del>A</del> TTTCAACA	4703
		TGTTAAAAGTAGCATAT	4704
		AGACTTATAATATTGTGGCTGCTCACGGTTATTTGGTCGATTAAT CTTCCAATATGCTACTTTAACAAATTCTCGTTCTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	4705
		CAGATCCCTACTACAGGCCAAGCAGCCAGAAAGAAGTGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCCAAAT AACCCTGAGCAGCCACAATATTATAAGTCT	4706
		ATATGCT <del>A</del> TTTCAACA	4707
20	Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	TGTTGAAAGTAGCATAT	4708
		AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCT <del>A</del> TTCAACAATTCTCGTTCTTACATTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTG	4709
		CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAT AACCCTGAGCAGCTACAATGTTGAAGTT	4710
		ATATGCT <del>A</del> TTTCAACA	4711
		TGTTGAAAGTAGCATAT	4712
25	Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCTACTTCAACAACCTCTCGTTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4713
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	4714
	ATATGCTACTTCAACA	4715
	TGTTGAAAGTAGCATAT	4716
10 Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCTACTTCAACAACCTCTCGCTCTTACATTCTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	4717
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAATGTAAAGAG CGAGAGTTGTTAAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCGGCTACGATATTATAAGTTT	4718
	ATATGCTACTTCAACA	4719
	TGTTAAAAGTAGCATAT	4720
15 Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCTACTTCAACAACCTCTCGTTCGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4721
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4722
	ATATGCTACTTCAACA	4723
	TGTTGAAAGTAGCATAT	4724
20 Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCTACTTCAACAATTCTCGTTCTTACATTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4725
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCAGCTACGATATTATAAGTTT	4726
	ATATGCTACTTCAACA	4727
	TGTTGAAAGTAGCATAT	4728
25 Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT	AAACCTTATAATTGAGCTCATGGTTATTTGGCGATTGAT CTTCCAATATGCTACTTCAACAACCTCTCGTTCTTACATTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4729
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAA TAACCATGAGCTGCTACAATTATAAGTTT	4730
	ATATGCTACTTCAACA	4731
	TGTTGAAAGTAGCATAT	4732

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCAAC <u>T</u> TCACA <u>A</u> CTCTCGTT <u>C</u> TTACATTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG	4733
		CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAA <u>A</u> TGTAAAGAA CGAGAATTGTTGAA <u>A</u> GTAGCATATTGGAAAGATCAATCGGCCAAAT AACCATGAGCAGCTACAATATTAGGTT	4734
		ATATGCA <u>A</u> CTTCACA	4735
		TGTTGAA <u>A</u> GTAGCATAT	4736
		AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCT <u>A</u> CTTCACA <u>A</u> CTCTCGTT <u>C</u> TTACATTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	4737
10	Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	CAAATACCTACTACCCGCCAAGCCGCTAAGAAGAA <u>A</u> TGTAAAGAA CGAGAATTGTTGAA <u>A</u> GTAGCATATTGGAAAGATCAATCGGCCAAAT AACCGTGAGCAGCTACAATGTTGAAGTT	4738
		ATATGCT <u>A</u> CTTCACA	4739
		TGTTGAA <u>A</u> GTAGCATAT	4740
		AAACTTATAATATTGTGGCCGCTCATGGTTATTTGGCCGATTAA <u>T</u> CTTCCAATATGCT <u>A</u> CTTCACA <u>A</u> CTCTCGTT <u>C</u> TTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTTG	4741
		CAAATCCCTACTACAGGCCAAGCAGCCAA <u>A</u> GAAGAAGTGTAAAGAA CGAGAGTTGTTAA <u>A</u> GTAGCATATTGGAAAGATTAATCGGCCAAAT AACCATGAGCGGCCACAATATTATAAGTT	4742
15	Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	ATATGCT <u>A</u> CTTCACA	4743
		TGTTAAA <u>A</u> GTAGCATAT	4744
		AGACTTATAATATTGTGGCTGCTCACGGTTATTTGGTCGATTAA <u>T</u> CTTCCAATATGCT <u>A</u> CTTCACA <u>A</u> CTCTCGTT <u>C</u> TTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	4745
		CAGATCCCTACTACAGGCCAAGCAGCCAA <u>A</u> GAAGAAGTGTAAAGAA CGAGAATTGTTGAA <u>A</u> GTAGCATATTGGAAAGATTAATCGACCAAAAT AACCGTGAGCAGCCACAATATTATAAGTCT	4746
		ATATGCT <u>A</u> CTTCACA	4747
20	Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	TGTTGAA <u>A</u> GTAGCATAT	4748
		AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT TTTCCAATATGCT <u>A</u> CTTCACA <u>A</u> CTCTCGTT <u>C</u> TTACATTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG	4749
		CAAATACCTACTACCCGCCAAGCCGCTAAGAAGAA <u>A</u> TGTAAAGAA CGAGAATTGTTGAA <u>A</u> GTAGCATATTGGAAAGATTAATCGACCAAAAT AACCGTGAGCAGCTACAATGTTGAAGTT	4750
		ATATGCT <u>A</u> CTTCACA	4751
		TGTTGAA <u>A</u> GTAGCATAT	4752
25	Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Triazine Resistant D1 Protein <i>Picea abies</i> Ser264Thr AGT-ACT	AAACCTACAATATTGTGGCTGCTCACGGTTATTCGGCCGATTGAT CTTCCAGTATGCTACTTCAACAACTCCCGTTCTTACATTCTTCT TAGCTGCTGGCCCGTAGCAGGTATCTG	4753
	CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGGGAGTTGTTGAAAGTAGCATACTGGAAGATCAATCGGCCAAA TAACCGTGAGCAGCCACAATATTGTAGGTT	4754
	GTATGCTACTTCAACA	4755
	TGTTGAAAGTAGCATA	4756
10 Triazine Resistant D1 Protein <i>Vicia faba</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTCGGCCGATTGAT CTTCCAATATGCTACTTCAACAAATTCTCGCTCTTACATTCTTCC TAGCTGCTGGCCTGTAGTAGGTATCTG	4757
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAAGTAGCATAATTGGAAGATCAATCGGCCAAAAT AACCCTGAGCAGCTACAATATTAGGTT	4758
	ATATGCTACTTCAACA	4759
	TGTTGAAAGTAGCATA	4760
	AGACTTATAATATTGTGGCTGCTCATGGTTATTCGGCCGATTAAT CTTCCAATATGCTACTTCAACAACTCTCGTTCTTACACTTCTTCT TGGCTGCTGGCCTGTAGTAGGAATCTG	4761
15 Triazine Resistant D1 Protein <i>Hordeum vulgare</i> Ser264Thr AGT-ACT	CAGATTCTACTACAGGCCAAGCAGCCAAGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATAATTGGAAGATTAATCGGCCAAAAT AACCAGGAGCAGCCACAATATTATAAGTCT	4762
	ATATGCTACTTCAACA	4763
	TGTTGAAAGTAGCATA	4764
	AAACTTATAATATTGTGGCTGCTCATGGTTATTCGGCCGATTAAT CTTCCAATATGCTACTTCAACAACTCTCGTTCTTACACTTCTTCT TGGCTGCTGGCCTGTAGTAGGAATCTG	4765
20 Triazine Resistant D1 Protein <i>Triticum aestivum</i> Ser264Thr AGT-ACT	CAGATTCTACTACAGGCCAAGCAGCCAAGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATAATTGGAAGATTAATCGGCCAAAAT AACCAGGAGCAGCCACAATATTATAAGTCT	4766
	ATATGCTACTTCAACA	4767
	TGTTGAAAGTAGCATA	4768
	AAACTTATAATATTGTAGCTGCTCATGGTTATTCGGCCGATTAATC TTCCAATATGCAACTTCAACAAATTCTCGTTCTTACATTCTTCT AGCTGCTGGCCTGTAGTAGGTATTG	4769
25 Triazine Resistant D1 Protein <i>Vigna unguiculata</i> Ser264Thr AGT-ACT	CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATAATTGGAAGATTAATCGGCCAAAAT AACCAGGAGCAGCTACAATATTATAAGTCT	4770
	ATATGCAACTTCAACA	4771
	TGTTGAAAGTAGCATA	4772

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Triazine Resistant D1 Protein <i>Lotus japonicus</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCAACTTCAACAACCTCTCGTTCTTACACTTCTCT TAGCTGCTTGGCCTGTTAGGTATCTG	4773
	CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAT AACCCTGAGCAGCTACAATATTAGGTTT	4774
	ATATGCAAC <u>TTT</u> CAACA	4775
	TGTTGAAAG <u>TT</u> GCATAT	4776
10 Triazine Resistant D1 Protein <i>Sinapis alba</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAATTCTCGTTCTTACATTCTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	4777
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAT AACCCTGAGCAGCTACAATATTAGGTTT	4778
	ATATGCT <u>ACTT</u> CAACA	4779
	TGTTGAAAGTAGCATAT	4780
15 Triazine Resistant D1 Protein <i>Pisum sativum</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAATTCTCGCTCTTACATTCTCC TAGCTGCTTGGCCTGTTAGTAGGTATCTG	4781
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAATGTAAAGAG CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAT AACCCTGAGCAGCTACAATATTAGGTTT	4782
	ATATGCT <u>ACTT</u> CAACA	4783
	TGTTGAAAGTAGCATAT	4784
20 Triazine Resistant D1 Protein <i>Spinacia oleracea</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTGGTCGATTGAT CTTCCAATATGCTACTTCAACAACCTCTCGTTCTTACACTTCTCT TAGCTGCTTGGCCTGTTAGTAGGTATTTG	4785
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGACCAAAAT AACCCTGAGCAGCTACGATATTATAAGTTT	4786
	ATATGCT <u>ACTT</u> CAACA	4787
	TGTTGAAAGTAGCATAT	4788
25 Triazine Resistant D1 Protein <i>Nicotiana debneyi</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAACCTCTCGTTCTTACACTTCTCC TAGCTGCTTGGCCTGTTAGTAGGTATCTG	4789
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAT TAACCCTGAGCGGCTACGATGTTATAAGTTT	4790
	ATATGCT <u>ACTT</u> CAACA	4791
	TGTTGAAAGTAGCATAT	4792

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Triazine Resistant D1 Protein <i>Solanum nigrum</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAACTCTCGTTGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4793
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTT	4794
	ATATGCTACTTCAACA	4795
	TGTTGAAAGTAGCATAT	4796
10 Triazine Resistant D1 Protein <i>Nicotiana</i> <i>plumbaginifolia</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTACTTCAACAACTCTCGTTGTTACACTTCTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4797
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTT	4798
	ATATGCTACTTCAACA	4799
	TGTTGAAAGTAGCATAT	4800

**Example 6**  
**Engineering male- or female-sterile plants**

Flower development in distantly related dicot plant species is increasingly better understood and appears to be regulated by a family of genes which encode regulatory proteins. These genes include, for example, *AGAMOUS* (*AG*), *APETALA1* (*AP1*), and *APETALA3* (*AP3*) and *P/STILLATA* (*P1*) in *Arabidopsis thaliana*, and *DEFICIENS A* (*DEFA*), *GLOBOSEA* (*GLO*), *SQUAMOSA* (*SQUA*), and *PLENA* (*PLE*) in *Antirrhinum majus*. Genetic studies have shown that the *DEFA*, *GLO* and *AP3* genes are essential for petal and stamen development. Sequence analysis of these genes revealed that the gene products contain a conserved MADS box region, a DNA-binding domain. Using these clones as probes, MADS box genes have also been isolated from other species including tomato, tobacco, petunia, *Brassica napus*, and maize.

Altering the expression of these genes results in altered floral morphology. For example, mutations in *AP3* and *P1* result in male-sterile flowers because petals develop in place of stamens.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer altered floral structures in plants.

**Table 14**  
**Oligonucleotides to produce male-sterile plants**

	<b>Phenotype, Gene, Plant &amp; Targeted Alteration</b>	<b>Altering Oligos</b>	<b>SEQ ID NO:</b>
20	Male-sterile <i>AP3</i> <i>Arabidopsis thaliana</i> Arg3Term AGA-TGA	TTGTCCTCTCCACCAAATCTCTCAACAAAAAGATTAACAAAGAGA GAAGAATATGGCGTGAGGGAGATCCAGATCAAGAGGATAGAGAA CCAGACAAACAGACAAGTGACGTATTCAA	4801
		TTGAATACGTCACTTGTCTGGTTCTATCCTCTTGATC TGGATCTTCCCTCACGCCATATTCTCTCTTTGTTAACATTTTT GTTGAAGAGAGATTGGTGGAGAGGGACAA	4802
		ATATGGCGTGAGGGAAAG	4803
		CTTCCCTCACGCCATAT	4804
		TCTCCACCAAATCTCTCAACAAAAAGATTAACAAAGAGAGAAGA ATATGGCGAGAGGGTAGATCCAGATCAAGAGGATAGAGAACCGAGA CAAACAGACAAGTGACGTATTCAAAGAGAA	4805
25	Male-sterile <i>AP3</i> <i>Arabidopsis thaliana</i> Lys5Term AAG-TAG	TTCTCTTGAATACGTCACTTGTCTGGTTCTATCCTC TTGATCTGGATCTACCCCTCGCCATATTCTCTCTTTGTTAACAT CTTTTGTTGAAGAGAGATTGGTGGAGA	4806
		CGAGAGGGTAGATCCAG	4807

	CTGGATCTACCCCTCTCG	4808
5	Male-sterile AP3 <i>Arabidopsis thaliana</i> Gln7Term CAG-TAG	CCAAATCTCTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGG CGAGAGGGAGATCTAGATCAAGAGGATAGAGAACCGACAAACA GACAAGTGACGTATTCAAAGAGAAGGAATG 4809
		CATTCCCTCTTGAATACGTCACTTGTCTGTTGTCTGGTTCTCT ATCCTCTTGATCTAGATCTCCCTCTGCCATATTCTCTCTTTG TTAATCTTTTGTGAAGAGATTGG 4810
		GGAAGATCTAGATCAAG 4811
		CTTGATCTAGATCTTCC 4812
		CTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAG GGAAGATCCAGATCTAGAGGATAGAGAACCGACAAACAGACAAG TGACGTATTCAAAGAGAAGGAATGGTTAT 4813
10	Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys9Term AAG-TAG	ATAAACCATCCCTCTTGAATACGTCACTTGTCTGTTGTCTGG TTCTCTATCCTCTAGATCTGGATCTCCCTCTGCCATATTCTCTC TCTTGTAACTTTGTGAAGAG 4814
		TCCAGATCTAGAGGATA 4815
		TATCCTCTAGATCTGGA 4816
		AGAGGGAAAGATCCAGATCAAGAGGATAGAGAACCGACCAACCGA CAAGTGACGTATTCTTAGAGAAGAAATGGTTGTCAAGAAAGCTC ACGAGCTTACAGTTTATGTGATGCTAGGG 4817
		CCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTCTTGAAACAA ACCATTCTCTCTAAGAATACGTCACTTGTGGTTGGTCTGGTTC TCTATCCTCTTGATCTGGATCTCCCTCT CGTATTCTTAGAGAAGA 4818
15	Male-sterile AP3 <i>Brassica oleracea</i> Lys23Term AAG-TAG	TCTTCTCTAAGAATACG 4819
		4820
		GGGAAGATCCAGATCAAGAGGATAGAGAACCGACCAACCGACAA GTGACGTATTCTAAGTAGAGAAATGGTTGTCAAGAAAGCTCACG AGCTTACAGTTTATGTGATGCTAGGGTT 4821
		AAACCCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTCTTGAA CAAACCATTTCTCCTAGAATACGTCACTTGTGGTTGGTCTGG TTCTCTATCCTCTTGATCTGGATCTCCC ATTCTAAGTAGAGAAAT 4822
		ATTCTTCACTTAGAAT 4823
20	Male-sterile AP3 <i>Brassica oleracea</i> Arg24Term AGA-TGA	ATTCTTCACTTAGAAT 4824
		AAGATCCAGATCAAGAGGATAGAGAACCGACCAACCGACAAAGTG ACGTATTCTAAGAGATGAAATGGTTGTCAAGAAAGCTCACGAGC TTACAGTTTATGTGATGCTAGGGTTCGA 4825
		TCGAAACCCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTCTT GAACAAACCATTTCTAGAATACGTCACTTGTGGTTGGTC TGGTTCTCTATCCTCTTGATCTGGATCTT 4826
		CTAAGAGATGAAATGGT 4827
		ACCATTCTCATCTCTTAG 4828
25	Male-sterile AP3 <i>Brassica oleracea</i> Arg25Term AGA-TGA	

5	Male-sterile AP3 <i>Brassica oleracea</i> Leu28Term TTG-TAG	TCAAGAGGATAGAGAACCAACCGACAAGTGACGTATTCTA AGAGAAGAAATGGTAGTTCAAGAAAGCTCACGAGCTTACAGTTT ATGTGATGCTAGGGTTTCGATTATCATGTT	4829
		AACATGATAATCGAACCTAGCATCACATAAAACTGTAAGCTCGT GAGCTTCTTGAACTAACCATTCTCTTAGAATACGTCACTTGT CGGTTGGTCTGGTTCTATCCTCTGA	4830
		AAATGGTAGTTCAAGA	4831
		TCTTGAACTAACCATT	4832
		GGCTCGAGGGAAAGATCCAGATTAAGAGGATAGAGAACCAAACAAA CAGGCAGGTCACCTAGTCCAAGAGAACGAAATGGTTGTTCAAGAA AGCACACGAGCTCTGTTCTGTGATGCT	4833
10	Male-sterile AP3 <i>Brassica napus</i> Tyr21Term TAC-TAG	AGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTGAACAAACC ATTTCTTCTCTGGACTAGGTGACCTGCCTGTTGTTGGTTCTA TCCTCTTAATCTGGATCTTCCCTCGAGCC	4834
		GTCACCTAGTCCAAGAG	4835
		CTCTTGGACTAGGTGAC	4836
		CGAGGGAAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGG CAGGTCACCTACTCCTAGAGAAGAAATGGTTGTTCAAGAAAGCAC ACGAGCTCTGTTCTGTGATGCTAAAG	4837
		CTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTGAACAA ACCATTCTCTAGGAGTAGGTGACCTGCCTGTTGTTGGTT TCTATCCTCTTAATCTGGATCTTCCCTCG	4838
15	Male-sterile AP3 <i>Brassica napus</i> Lys23Term AAG-TAG	CCTACTCCTAGAGAAGA	4839
		TCTTCTCTAGGAGTAGG	4840
		GGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAGTGAAGAAATGGTTGTTCAAGAAAGCACACG AGCTCTGTTCTGTGATGCTAAAGTTT	4841
		AAACTTCTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTGAA CAAACCATTCCTCACTGGAGTAGGTGACCTGCCTGTTGTTGG TTCTCTATCCTCTTAATCTGGATCTTCCC	4842
		ACTCCAAGTGAAGAAAT	4843
20	Male-sterile AP3 <i>Brassica napus</i> Arg24Term AGA-TGA	ATTCTTCACTGGAGT	4844
		AAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTC ACCTACTCCAAGAGATGAAATGGTTGTTCAAGAAAGCACACGAGC TCTCTGTTCTGTGATGCTAAAGTTCCA	4845
		TGGAAACTTCTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTCTT GAACAAACCATTCATCTCTGGAGTAGGTGACCTGCCTGTTGTT TGGTTCTCTATCCTCTTAATCTGGATCTT	4846
		CCAAGAGATGAAATGGT	4847
		ACCATTTCATCTCTGG	4848
25	Male-sterile AP3 <i>Brassica napus</i> Arg25Term AGA-TGA		

5	Male-sterile DEFA <i>Antirrhinum majus</i> Arg3Term CGA-TGA	GGAGAGAAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGT AGTGGTTCGATGGCTTGAGGGAAGATCCAGATTAAGAGGATAGAG AACCAAACAAACAGGCAGGTACCTACTCCA	4849
		TGGAGTAGGTGACCTGCCTGTTGTTGGTCTCTATCCTCTTAAT CTGGATCTCCCTCAAGCCATCGAACCACTACCAACTGCTCTG TTTCTTCTCCAGCTTCCTTCTCTCC	4850
		CGATGGCTTGAGGGAAG	4851
		CTTCCCTCAAGCCATCG	4852
10	Male-sterile DEFA <i>Antirrhinum majus</i> Lys5Term AAG-TAG	AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGT TCGATGGCTCGAGGGTAGATCCAGATTAAGAGGATAGAGAACCAA ACAAACAGGCAGGTACCTACTCCAAGAGAA	4853
		TTCTCTGGAGTAGGTGACCTGCCTGTTGTTGGTCTCTATCCT CTTAATCTGGATCTACCCCTCGAGCCATCGAACCACTACCAACTG CTCTGTTCTTCTCCAGCTTCCTT	4854
		CTCGAGGGTAGATCCAG	4855
		CTGGATCTACCCCTCGAG	4856
15	Male-sterile DEFA <i>Antirrhinum majus</i> Gln7Term CAG-TAG	AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATG GCTCGAGGGAAGATCTAGATTAAGAGGATAGAGAACCAAACAAAC AGGCAGGTACCTACTCCAAGAGAAATG	4857
		CATTTCTCTTGGAGTAGGTGACCTGCCTGTTGTTGGTCTC TATCCTCTTAATCTAGATCTCCCTCGAGCCATCGAACCACTACCA CTACTGCTCTGTTCTTCTCCAGCTT	4858
		GGAAGATCTAGATTAAG	4859
		CTTAATCTAGATCTCC	4860
20	Male-sterile DEFA <i>Antirrhinum majus</i> Lys9Term AAG-TAG	GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGA GGGAAGATCCAGATTAGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAGAGAAGAAATGGTTGT	4861
		ACAAACCATTTCTCTTGGAGTAGGTGACCTGCCTGTTGTTG GTTCTCTATCCTCTAAATCTGGATCTCCCTCGAGCCATCGAACCA CTACCACTACTGCTCTGTTCTTC	4862
		TCCAGATTAGAGGATA	4863
		TATCCTCTAAATCTGGA	4864
25	Male-sterile AP3 <i>Nicotiana tabacum</i> Lys5Term AAG-TAG	TCAGTAATTCTAAGATCTCAAACCTTGAGCAAAAGAAAAAAAC TATGGCTCGTGGTAGATCCAGATCAAGAGAATAGAGAACCAAAC AAACAGACAAGTCACCTATTCTAAGAGAA	4865
		TTCTCTAGAATAAGTGACTTGTCTGTTGTTGGTCTCTATTCTC TTGATCTGGATCTACCCACGAGCCATAGTTTTTTCTTTTGCTC AAAGTTGAGATCTAAGAATTACTGA	4866
		CTCGTGGGTAGATCCAG	4867
		CTGGATCTACCCACGAG	4868

5	Male-sterile AP3 <i>Nicotiana tabacum</i> Gln7Term CAG-TAG	ATTCTTAAGATCTAAACTTTGAGCAAAAGAAAAAAACTATGGC TCGTGGGAAGATCTAGATCAAGAGAATAGAGAACCAACAAACAGA CAAGTCACCTATTCTAAGAGAAGAAATG	4869
		CATTTCTCTCTAGAATAAGTGA <del>CTTGACTGTCTGTTGGT</del> CTCT ATTCTCTGATCTAGATCTTCCCACGAGCCATAGTTTTTTCTTT TTGCTCAAAGTTGAGATCTAAGAAT	4870
		GGAAGATCTAGATCAAG	4871
		CTTGTATCTAGATCTTCC	4872
10	Male-sterile AP3 <i>Nicotiana tabacum</i> Lys9Term AAG-TAG	AAGATCTCAAACTTGAGCAAAAGAAAAAAACTATGGCTCGTG GGAAGATCCAGATCTAGAGAATAGAGAACCAACAAACAGACAAGT CACTTATTCTAAGAGAAGAAATGGACTTT	4873
		AAAGTCCATTCTCTCTAGAATAAGTGA <del>CTTGACTGTCTGTTGG</del> TTCTCTATTCTCTAGATCTGGATCTTCCCACGAGCCATAGTTTTTT TTCTTTTGCTCAAAGTTGAGATCTT	4874
		TCCAGATCTAGAGAATA	4875
		TATTCTCTAGATCTGGA	4876
		ATCTCAAACTTGAGCAAAAGAAAAAAACTATGGCTCGGG AGATCCAGATCAAGTGA <del>ATAGAGAACCAACAAACAGACAAGTCAC</del> TTATTCTAAGAGAAGAAATGGACTTTCA	4877
15	Male-sterile AP3 <i>Nicotiana tabacum</i> Arg10Term AGA-TGA	TGAAAAGTCATTCTCTCTAGAATAAGTGA <del>CTTGACTGTCTGTTGG</del> TGGTTCTCTATTCA <del>CTGATCTGGATCTTCCCACGAGCCATAGTT</del> TTTTTCTTTGCTCAAAGTTGAGAT	4878
		AGATCAAGTGAATAGAG	4879
		CTCTATTCA <del>CTGATCT</del>	4880
		GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAAACGAA CAGACAAGTAAC <del>TAGTCAAACG</del> AAGGGATGGTCTTTCAAGAAG GCCAATGAGCTCACTGTTCTTGATGCT	4881
		AGCATCACAAAGAACAGTGA <del>GCTATTGGCCTTCTGAAAAGACCA</del> TCCCTTCGTTTGACTAAGTTACTGTC <del>GTTCGTTGTGTTCTAT</del> TCTCTTGATCTGGATCTTCCTCGAGCC	4882
20	Male-sterile AP3 <i>Medicago sativa</i> Tyr21Term TAC-TAG	GTAAC <del>TTAGTCAAACG</del>	4883
		CGTTTGACTAAGTTAC	4884
		CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAAACGAA GACAAGTAAC <del>TACTGAAAACG</del> AAGGGATGGTCTTTCAAGAAGGC CAATGAGCTCACTGTTCTTGATGCTAA	4885
		TTAGCATCACAAAGAACAGTGA <del>GCTATTGGCCTTCTGAAAAGAC</del> CATCCCTTCGTTTGACTAAGTTACTGTC <del>GTTCGTTGTGTTCT</del> ATTCTCTTGATCTGGATCTTCCTCGAG	4886
		AACTTACTGAAAACGAA	4887
25	Male-sterile AP3 <i>Medicago sativa</i> Ser22Term TCA-TGA	TTCGTTTGACTAAGTT	4888

5	Male-sterile AP3 <i>Medicago sativa</i> Lys23Term AAA-TAA	CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGA CAAGTAACCTACTCATACGAAGGGATGGCTTTCAAGAAGGCCA ATGAGCTCACTGTTCTTGTGATGCTAAGG	4889
	CCTTAGCATCACAAAGAACAGTGAGCTATTGGCCTTCTGAAAAG ACCATCCCTCGTTATGAGTAAGTTACTTGTCTGTTGTGTTCT	4890	
	CTATTCTCTGATCTGGATCTTCCTCG		
	CTTACTCATACGAAGG	4891	
10	Male-sterile AP3 <i>Medicago sativa</i> Arg24Term CGA-TGA	CCTTCGTTATGAGTAAG	4892
		GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAA GTAACCTACTCAAATGAAGGGATGGCTTTCAAGAAGGCCAATG AGCTCACTGTTCTTGTGATGCTAAGGTT	4893
		AAACCTTAGCATCACAAAGAACAGTGAGCTATTGGCCTTCTGAA AAGACCATCCCTCATTTGAGTAAGTTACTTGTCTGTTGTGTT	4894
		TCTCTATTCTCTGATCTGGATCTTC	
		ACTCAAATGAAGGGAT	4895
15	Male-sterile DEF4 <i>Solanum tuberosum</i> Tyr21Term TAT-TAG	ATCCCTTCATTTGAGT	4896
		GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAAT AGGCAAGTGACTTAGTCAAAGAGAAGAAATGGGCTATTCAAGAAG GCTAATGAACCTACAGTTCTTGTGATGCT	4897
		AGCATCACAAAGAACTGTAAGTTCAATTAGCCTTCTGAAATAGCCC TTTCTCTCTTGAAGTCACTTGCCTATTGTTGGTTTCTATT	4898
		TTCTTGATCTGGATCTTACCAACGAGCC	
		GTGACTTAGTCAAAGAG	4899
20	Male-sterile DEF4 <i>Solanum tuberosum</i> Ser22Term TCA-TGA	CTCTTTGACTAAGTCAC	4900
		CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAG GCAAGTGACTTATTGAAAGAGAAGAAATGGGCTATTCAAGAAGGCT AATGAACCTACAGTTCTTGTGATGCTAA	4901
		TTAGCATCACAAAGAACTGTAAGTTCAATTAGCCTTCTGAAATAGCC CATTCTCTCTTCAATAAGTCACTTGCCTATTGTTGGTTTCTA	4902
		TTTCTTGATCTGGATCTTACCAACGAG	
		GACTTATTGAAAGAGAA	4903
25	Male-sterile DEF4 <i>Solanum tuberosum</i> Lys23Term AAG-TAG	TTCTCTTCATAAGTC	4904
		CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGC AAGTGACTTATTCAAGAGAAGAAATGGGCTATTCAAGAAGGCTAA TGAACCTACAGTTCTTGTGATGCTAAAG	4905
		CTTAGCATCACAAAGAACGTAAGTTCAATTAGCCTTCTGAAATAGC CCATTCTCTCTATGAATAAGTCACTTGCCTATTGTTGGTTTCTA	4906
		TATTTCTTGATCTGGATCTTACCAACG	
		CTTATTCAAGAGAAGA	4907
		TCTTCTCTATGAATAAG	4908

5	Male-sterile DEF4 <i>Solanum tuberosum</i> Arg24Term AGA-TGA	GGTAAGATCCAGATCAAGAAAATAGAAAACCAACAAATAGGCAAG TGACTTATTCAAAGTGAAGAAAATGGGCTATTCAAGAAGGCTAATGA ACTTACAGITCTTGATGCTAAAGTTT	4909
		AAACTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAAT AGCCCATTCTTCACTTGAATAAGTCACTTGCCTATTGTTGGTT TTCTATTCTTGATCTGGATCTTACCT	4910
		ATTCAAAGTGAAGAAAAT	4911
		ATTCTTCACTTGAAT	4912
		GCTAATGAACCTACTGTTCTTGATGCTAAAGTTCAATTGTTAT GATTCTAGTACTTGAAGAAACTTCATGAGTTATAAGTCCCTCTATCA CGACCAAAACAATTGTTCGATCTGTACC	4913
10	Male-sterile AP3 <i>Lycopersicon esculentum</i> Gly27Term GGA-TGA	GGTACAGATCGAACAAATTGTTGGTCGTGATAGAGGGACTTATAAA CTCATGAAGTTTCAAGTACTAGAAATCATAACAATTGAAACTTAG CATCACAAAGAACAGTAAGTTCATTAGC	4914
		CTAGTACTTGAAGAAACTT	4915
		AAGTTTCAAGTACTAG	4916
		AATGAACCTACTGTTCTTGATGCTAAAGTTCAATTGTTATGAT TTCTAGTACTGGATAACTTCATGAGTTATAAGTCCCTCTATCACGA CCAAACAATTGTTCGATCTGTACCAGA	4917
		TCTGGTACAGATCGAACAAATTGTTGGTCGTGATAGAGGGACTTAT AAACTCATGAAGTTATCCAGTACTAGAAATCATAACAATTGAAACTT TAGCATCACAAAGAACAGTAAGTTCATT	4918
15	Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys28Term AAA-TAA	GTACTGGATAACTTCAT	4919
		ATGAAGTTATCCAGTAC	4920
		ACTGTTCTTGATGCTAAAGTTCAATTGTTATGATTCTAGTAC TGGAAAACCTCATAGTTATAAGTCCCTCTATCACGACCAAACAAT TGTTCGATCTGTACCAGAACAGTATTG	4921
		CAATAGTCTTCTGGTACAGATCGAACAAATTGTTGGTCGTGATAGA GGGACTTATAAAACTATGAAGTTCCAGTACTAGAAATCATAACAA TTGAAACTTAGCATCACAAAGAACAGT	4922
		AACTTCATAGTTATA	4923
20	Male-sterile AP3 <i>Lycopersicon esculentum</i> Glu31Term GAG-TAG	TATAAAACTATGAAGTT	4924
		ATTGTTATGATTCTAGTACTGGAAAACCTCATGAGTTATAAGTCC CTCTATCACGACCTAACAAATTGTTCGATCTGTACCAGAACAGTATT GGAGTTGATATTGGACTACTCACTATG	4925
		CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTCTGGTACAG ATCGAACAAATTGTTAGGTCGTGATAGAGGGACTTATAAACTCATGA AGTTTCCAGTACTAGAAATCATAACAAAT	4926
		TCACGACCTAACAAATTG	4927
		CAATTGTTAGGTCGTGA	4928
25	Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys40Term AAA-TAA		

5	Male-sterile AP3 <i>Triticum aestivum</i> Tyr21Term TAC-TAG	GGGGCGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCA ACAGGCAGGTGACCT <u>AGT</u> CCAAGCGCCGGTCGGGGATCATGAAG AAGGCAGGGAGCTACCGTGC <u>CT</u> CGACGCC	4929
		GGCGTCGAGAGCACGGTGAGCTCCCGCGC <u>TTCTT</u> CATGATCC CCGACCGGGC <u>GT</u> GGACTAGGT <u>CA</u> CTGCC <u>TTGGTGGCGT</u> TC TCGATCCG <u>TTT</u> ATCTCAAT <u>CTTCCCCGCCCC</u>	4930
		GTGAC <u>CTAGT</u> CCAAGCG	4931
		CGCTTGG <u>ACTAGGT</u> CAC	4932
10	Male-sterile AP3 <i>Triticum aestivum</i> Lys23Term AAG-TAG	CGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAG GCAGGTGAC <u>CTACTCC</u> <u>TA</u> GC <u>GGCGGTC</u> GGATCATGAAGAAGG CCGGGGAG <u>CTACCGTGC</u> CTGC <u>ACGCCAGG</u>	4933
		CCTGGCG <u>TCGAGAGCACGGTGAGCTCCCGCGC</u> <u>TTCTT</u> CATG AT <u>CCCCGACC</u> GGCG <u>CTAGGAGTAGGT</u> CAC <u>CTGCC</u> <u>TTGGTGGC</u> GTT <u>CTCGATCCG</u> <u>TTT</u> ATCTCAAT <u>CTTCCCCG</u>	4934
		CCT <u>ACTCC</u> <u>TA</u> GC <u>GCCGG</u>	4935
		CCGGCG <u>CTAGGAGTAGG</u>	4936
15	Male-sterile AP3 <i>Triticum aestivum</i> Ser26Term TCG-TAG	TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCT ACT <u>CCAAGCGCCGGT</u> <u>A</u> GGGGATCATGAAGAAGGCG <u>GGGAGCT</u> ACCGTG <u>CTGC</u> GACGCC <u>AGGTG</u> CC <u>ATCAT</u>	4937
		ATGATGG <u>CGAC</u> CTGG <u>CGTC</u> GG <u>AGAGCACGGT</u> GAG <u>CTCCGCGC</u> CTT <u>CTT</u> CAT <u>GA</u> CC <u>CT</u> <u>ACCGGC</u> G <u>CTTGGAGTAGGT</u> CAC <u>CTGC</u> C <u>CT</u> GTTGG <u>GGCG</u> <u>TTCTCG</u> <u>ATCCG</u> <u>CTT</u> AT <u>CTCAA</u>	4938
		GCG <u>CCGGT</u> <u>AGGG</u> AT <u>CA</u>	4939
		TGAT <u>CCCC</u> <u>CTACCGG</u> <u>CGC</u>	4940
20	Male-sterile AP3 <i>Triticum aestivum</i> Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACAGGCAGGTGAC <u>CTACTCC</u> AAGCG CCGGT <u>CGGG</u> AT <u>CATG</u> T <u>AGAAGGCG</u> CG <u>GGAGCTACCGT</u> G <u>CT</u> GCG <u>ACGCC</u> <u>AGGTG</u> <u>CC</u> <u>ATCAT</u> <u>ATG</u> <u>TTCTC</u> <u>CT</u>	4941
		AGGAGAAC <u>ATG</u> <u>ATG</u> <u>GGCG</u> <u>AC</u> CTGG <u>CGTC</u> GG <u>AGAGCACGGT</u> AG <u>CTCCGCGC</u> <u>TTCT</u> <u>AC</u> <u>ATG</u> <u>ATCCCCGACC</u> GG <u>CGCTTGGAGTA</u> GGT <u>CAC</u> CT <u>GC</u> <u>CTG</u> <u>TTGGTGGCG</u> <u>TTCTCG</u> <u>ATCCG</u>	4942
		GG <u>ATCATG</u> <u>TA</u> GAAGGCG	4943
		CG <u>CC</u> <u>TTCT</u> <u>AC</u> <u>ATG</u> <u>ATCC</u>	4944
25	Male-sterile Silky1 <i>Zea mays</i> Tyr21Term TAC-TAG	GGGGCGGG <u>CAAG</u> AT <u>CGAGA</u> TC <u>AGCGG</u> AT <u>CGAGAACGCCACCA</u> ACCG <u>CCAGGTG</u> <u>AC</u> CT <u>AGT</u> CCA <u>AGCGCCGG</u> <u>ACGGGG</u> AT <u>CATG</u> AAG AAGG <u>CACCG</u> <u>GAGC</u> TC <u>ACCGT</u> <u>GC</u> <u>CTGC</u> <u>ACGCC</u>	4945
		GGCG <u>TCGAGAGCACGGT</u> <u>GAGCTCGCG</u> <u>CGCTTCTT</u> CATGATCC CCG <u>TCCGGCG</u> <u>CTTGG</u> <u>ACTAGGT</u> <u>CAC</u> CT <u>GGCGG</u> <u>TTGGTGGCG</u> <u>TC</u> TCGAT <u>CCG</u> <u>TTG</u> <u>ATCTCG</u> <u>ATCTGCC</u> <u>GGCCCC</u>	4946
		GTGAC <u>CTAGT</u> CCAAGCG	4947
		CGCTTGG <u>ACTAGGT</u> CAC	4948

5	Male-sterile Silky1 <i>Zea mays</i> Lys23Term AAG-TAG	CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCG CCAGGTGACCTACTCCTAGCCCCGGACGGGGATCATGAAGAAGG CACCGAGCTCACCGTGCTCTGCACGCCAGG	4949
		CCTGGGCGTCGCAGAGCACGGTGAGCTCGCGCCTTCTTCATG ATCCCCGTCGGCGCTAGGAGTAGGTACACCTGGCGGTTGGTGGC GTTCTCGATCCGCTTGTATCTCGATCTGCCGCG	4950
		CCTACTCCTAGCGCCGG	4951
		CCGGCGCTAGGAGTAGG	4952
		CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCG CCGGACGGGGATCATGTAGAAGGCACCGAGCTACCGTGCTCT CCGACGCCAGGTGCCATCATCATGTTCTCCT	4953
10	Male-sterile Silky1 <i>Zea mays</i> Lys30Term AAG-TAG	AGGAGAACATGATGATGGCGACCTGGCGTGCAGAGCACGGTG AGCTCGCGTGCCTCTCATGATCCCCGTCCGGCGCTTGGAGTAG GTCACCTGGCGGTTGGCGCTTCGATCCG	4954
		GGATCATGTAGAAGGCA	4955
		TGCCTTCTACATGATCC	4956
		ATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCG GACGGGGATCATGAAGTAGGCACCGAGCTACCGTGCTCTGCG ACGCCAGGTGCCATCATCATGTTCTCCTCCA	4957
15	Male-sterile Silky1 <i>Zea mays</i> Lys31Term AAG-TAG	TGGAGGAGAACATGATGATGGCGACCTGGCGTGCAGAGCACG GTGAGCTCGCGTGCCTACTTCATGATCCCCGTCCGGCGCTTGG GTAGGTCACCTGGCGGTTGGTGGCGTTCTCGAT	4958
		TCATGAAGTAGGCACGC	4959
		GCGTGCCTACTTCATGA	4960
		GCTAGCTGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGC GGCCATGGGGAGGGGCTAGATCGAGATCAAGCGGATCGAGAACG CGACCAACAGGCAGGTGACCTACTCGAACGC	4961
20	Male-sterile AP3 <i>Oryza sativa</i> Lys5Term AAG-TAG	GGCGCTTCGAGTAGGTACCTGCCTGTTGGTGCCTCGATCC GCTTGATCTCGATCTAGCCCCCTCCCATGGCCGCCCGCTGCAGC AGCTATCTCTCGCCGGACAATGCAGCTAGC	4962
		GGAGGGGCTAGATCGAG	4963
		CTCGATCTAGCCCCCTCC	4964
		TGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCAT GGGGAGGGGCAAGATCTAGATCAAGCGGATCGAGAACCGCACCG ACAGGCAGGTGACCTACTCGAACCGCCGCACGG	4965
25	Male-sterile AP3 <i>Oryza sativa</i> Glu7Term GAG-TAG	CCGTGCGGGCGCTTCGAGTAGGTACCTGCCTGTTGGTGCCT CGATCCGCTTGTATCTAGATCTTGCCTCCCCATGGCCGCCCG GCAGCAGCTATCTCTCGCCGGACAATGCA	4966
		GCAAGATCTAGATCAAG	4967
		CTTGATCTAGATCTGC	4968

5	Male-sterile AP3 <i>Oryza sativa</i> Lys9Term AAG-TAG	GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGA GGGGCAAGATCGAGATCTAGCGGATCGAGAACGCGACCAACAGG CAGGTGACCTACTCGAAGCGCCGACGGGATCA	4969
		TGATCCCCGTGCGGCCTCGAGTAGGTCACCTGCCTGTTGGTC GCGTCTCGATCCGCTAGATCTCGATCTGCCCTCCCATGGCC	4970
		GCCCCCTGCAGCAGCTATCTCTCGCCGGAC	
		TCGAGATCTAGCGGATC	4971
10	Male-sterile AP3 <i>Oryza sativa</i> Glu12Term GAG-TAG	GATCCGCTAGATCTGA	4972
		GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGAGGGCAAGA TCGAGATCAAGCGGATCTAGAACGCGACCAACAGGCAGGTGACCT	4973
		ACTCGAAGCGCCGACGGGATCATGAAGAAGG	
		CCTTCTTCATGATCCCCGTGCGCGCTTCGAGTAGGTCACCTGCC TGTTGGTCGCGTTCTAGATCCGCTTGTCTCGATCTGCCCTCC	4974
		CCATGGCCGCCCTGCAGCAGCTATCTC AGCGGATCTAGAACGCG	4975
		CGCGTTCTAGATCCGCT	4976

**Table 15**  
**Oligonucleotides to produce male-sterile plants**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
15	Male-sterile AG <i>Arabidopsis thaliana</i> Tyr35Term TAC-TAG	TCTGTACTAATCAAATTTCGCCCTAACGTTTGGCTTGGAGCA GCAATCACGGCGTAGCAATCGGAGCTAGGAGGAGATTCCCTCTCC CTTGAGGAAATCTGGGAGAGGAAAGATCGAA	4977
		TTCGATCTTCCTCTCCAGATTCCCTCAAGGGAGAGGAATCTCCT CCTAGCTCCGATTGCTACGCCGTGATTGCTGCTCAAAGCCAAA	4978
		ACGTTAGGGCAAAATTGATTAGTACAGA	4979
		TCCGATTGCTACGCCGT	4980
20	Male-sterile AG <i>Arabidopsis thaliana</i> Gln36Term CAA-TAA	CTGTACTAATCAAATTTCGCCCTAACGTTTGGCTTGGAGCAG CAATCACGGCGTACTAATCGGAGCTAGGAGGAGATTCCCTCTCC TGAGGAAATCTGGGAGAGGAAAGATCGAA	4981
		TTTCGATCTTCCTCTCCAGATTCCCTCAAGGGAGAGGAATCTCC TCCTAGCTCCGATTAGTACGCCGTGATTGCTGCTCAAAGCCAAA	4982
		AACGTTAGGGCAAAATTGATTAGTACAG	
		CGGCGTACTAATCGGAG	4983
		CTCCGATTAGTACGCCG	4984

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile AG <i>Arabidopsis thaliana</i> Ser37Term TCG-TAG	ACTAATCAAATTTGCCCTAACGTTTGGCTTGAGCAGCAAT CACGGCGTACCAAT <u>AGGAGCTAGGAGGAGATTCCCTCCCTTGA</u> GGAAATCTGGGAGAGGAAGATCGAAATCAA	4985
		TTGATTTCGATCTTCCTCTCCAGATTCTCAAGGGAGAGGAAT CTCCTCCTAGCTCT <u>ATTGGTACGCCGTGATTGCTGCTCCAAAGC</u> CAAAAACGTTAGGGCAAATTGATTAGT	4986
		GTACCAAT <u>AGGAGCTAG</u>	4987
		CTAGCTCC <u>ATTGGTAC</u>	4988
10	Male-sterile AG <i>Arabidopsis thaliana</i> Glu38Term GAG-TAG	TAATCAAATTTGCCCTAACGTTTGGCTTGAGCAGCAATCA CGGGCGTACCAAT <u>CGTAGCTAGGAGGAGATTCCCTCCCTTGAGGA</u> AATCTGGGAGAGGAAGATCGAAATCAAAC	4989
		GTTTGAATTCGATCTTCCTCTCCAGATTCTCAAGGGAGAGGA ATCTCCTCCTAGCT <u>ACGATTGGTACGCCGTGATTGCTGCTCCAA</u> GCCAAAAACGTTAGGGCAAATTGATTA	4990
		ACCAAT <u>CGTAGCTAGGA</u>	4991
		TCCTAGCT <u>ACGATTGGT</u>	4992
		CTCTCCCACITCTTTGGTGGTTATTCATTGGTACCGATATCA CAGAAGCAATGG <u>TAAGGTGGAGTAGTCACGATGCAGAGAGTA</u> GCAAGAAGATAGGTAGAGGGAAAGATAGAGA	4993
15	Male-sterile AG <i>Brassica napus</i> Glu3Term GAA-TAA	TCTCTATCTCCCTACCTATCTCTTGACTCTGCATCGT ACTACTCCCACCT <u>TAATCCATTGCTCTGTGATATCGTCACCAAAT</u> GAATAAACACC <u>GAAAAGAAGTGGGAGAG</u>	4994
		CAATGGATT <u>AAAGGTGGG</u>	4995
		CCCACCT <u>TAATCCATTG</u>	4996
		TATTCA <u>TTGGTACGATATCACAGAAGCAATGGATGAAGGTGGG</u> AGTAGTCACGAT <u>GCATAGAGTAGCAAGAAGATAGGTAGAGGGAAAG</u> ATAGAGATA <u>AAAGAGGATAGAGAACACAACAA</u>	4997
		TTGTTGTGTTCTATCCTCTTATCTCTATCTACCTATC TTCTTGCTACT <u>CTATGCATCGT</u> GACTACTCCCACCTTCATCCATTG CTTCTGTGATATCGTCACCAATGAATA	4998
20	Male-sterile AG <i>Brassica napus</i> Glu11Term GAG-TAG	ACGAT <u>GCATAGAGTAGC</u>	4999
		GCTACT <u>CTATGCATCGT</u>	5000
		GGTGACGATATCACAGAAGCAATGGATGAAGGTGGAGTAGTCA CGAT <u>GCAGAGAGTAGCTAGAAGATAGGTAGAGGGAAAGATAGAGAT</u> AAAGAGGATAGAGAACACAACAA <u>ATCGTCAAG</u>	5001
		CTTGACGATTGTTGTTCTATCCTCTTATCTCTATCTACCT CTACCTATCT <u>CTAGCTACTCTGCATCGT</u> GACTACTCCCACCTT CATCCATTGCTCTGTGATATCGTCACC	5002
		AGAGTAG <u>CTAGAAGATA</u>	5003
25	Male-sterile AG <i>Brassica napus</i> Lys14Term AAG-TAG	TATCTT <u>CTAGCTACTCT</u>	5004

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile AG <i>Brassica napus</i> Lys15Term AAG-TAG	GACGATATCACAGAACGATGGATGAAGGTGGAGTAGTCACGAT GCAGAGAGTAGCAAGTAGATAGGTAGAGGGAAAGATAGAGATAAAG AGGATAGAGAACACAACAAATCGTCAAGTAA	5005
		TTACTTGACGATTGTTGTTCTATCCTCTTATCTCTATCTTC CCTCTACCTATCT <u>A</u> CTTGCTACTCTCTGCATCGTGACTACTCCAC CTTCATCCATTGCTCTGTGATATCGTC	5006
		GTAGCAAGTAGATAGGT	5007
		ACCTATCT <u>A</u> CTTGCTAC	5008
10	Male-sterile AG <i>Lycopersicon esculentum</i> Glu4Term CAA-TAA	CAACCAAAAAACTAAAAATCTTCTCTTCCCTTACAAGGTGA AGTAATGGACTT <u>C</u> TAAAGTGATCTAACCAAGAGAGATCTCACCACAA AGGAAACTAGGAAGGGGGAAAATTGAGA	5009
		TCTCAATTTCCTCCCTAGTTCCCTTGTGGTAGATCTCT GGTTAGATCACT <u>T</u> AGAAGTCCATTACTCACCTTGTAAGGAAAGG AAAGAGAAGATTTAAGTTTTGGTT	5010
		TGGACTT <u>C</u> AAAGTGAT	5011
		ATCACT <u>T</u> AGAAGTCCA	5012
15	Male-sterile AG <i>Lycopersicon esculentum</i> Arg9Term AGA-TGA	AAAATCTTCTCTTCCCTTACAAGGTGAAGTAATGGACTTCC AAAGTGATCTAAC <u>C</u> TGAGAGATCTCACCACAAAGGAAACTAGGAA GGGGAAAATTGAGATCAAAGGATCGAAA	5013
		TTTCGATCTTTGATCTCAATTTCCTCCCTAGTTCCCTTGT GGTGAGATCT <u>C</u> AGGTTAGATCACTTGGAAGTCCATTACTCAC CTTGTAGGAAAGGAAAGAGAAGATTT	5014
		ATCTAAC <u>C</u> TGAGAGATC	5015
		GATCTCT <u>C</u> AGGTTAGAT	5016
20	Male-sterile AG <i>Lycopersicon esculentum</i> Glu10Term GAG-TAG	ATCTTCTCTTCCCTTACAAGGTGAAGTAATGGACTTCCAAA GTGATCTAAC <u>C</u> AGATAGATCTCACCACAAAGGAAACTAGGAAGGG GGAAAATTGAGATCAAAGGATCGAAAACA	5017
		TGTTTCGATCTTTGATCTCAATTTCCTCCCTAGTTCCCTT TGTGGTAGAGAT <u>T</u> ACTGGTTAGATCACTTGGAAGTCCATTACT CACCTGTAGGAAAGGAAAGAGAAGAT	5018
		TAACCAGATAGATCTCA	5019
		TGAGAT <u>T</u> ACTGGTTA	5020
25	Male-sterile AG <i>Lycopersicon esculentum</i> Ser12Term TCA-TGA	CTTCCCTTCCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCT AACCAAGAGAGAT <u>C</u> TGACCACAAAGGAAACTAGGAAGGGGGAAAAT TGAGATCAAAGGATCGAAAACACGACGAA	5021
		TTCGTCGTGTTCGATCTTGTGATCTCAATTTCCTCCCTA GTTCCCTTGTGGTCAGATCTCTGGTTAGATCACTTGGAAGTC CATTACTCACCTGTAGGAAAGGAAAG	5022
		AGAGAT <u>T</u> GACCACAA	5023

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	TTTGTGGTCAGATCTCT	5024
	Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln4Term CAA-TAA	GTA AAGTATGGACTCTAAAGTGATCTAACAGAGAGATCTCCACAA AGGAAACTGGGAAGAGGAAGATTGAGA
		TCTCAATCTTCTCTCCAGTTCTTGAGAGATCTCTCT TGTTAGATCACTTTAGAAGTCATACTTACACCTGGTAAGGAAAGA
		AAGGGTTGGAAGATGAAAATAGAGAGTAC
		TGGACTTCTAAAGTGAT
10	Male-sterile NAG1 <i>Nicotiana tabacum</i> Arg9Term AGA-TGA	ATCACTTTAGAAGTCCA
		ATCTTCCAACCCCTTCTTCTTACCA AAAGTGATCTAACATGAGAGATCTCTCCACAAAGGAAACTGGGAA GAGGAAAGATTGAGATCAAACGGATCGAAA
		TTTCGATCCGTTGATCTCAATCTTCTTCCAGTTCTTGT GGAGAGATCTCTCATGTTAGATCACTTGGAAAGTCCATACTTCAC CTGGTAAGGAAAGAAAGGGTTGGAAGAT
		ATCTAACATGAGAGATC
		GATCTCTCATGTTAGAT
15	Male-sterile NAG1 <i>Nicotiana tabacum</i> Glu10Term GAG-TAG	5029
		ATCTAACACAGGATCGAAACAA GAAAGATTGAGATCAAACGGATCGAAAACA
		TGTGGAGAGATCTATCTTGTAGATCACTTGGAAAGTCCATACTTT CACCTGGTAAGGAAAGAAAGGGTTGGA
		TAACAAGAGATCTCT
		AGAGATCTATCTTGTAA
20	Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln14Term CAA-TAA	5030
		5031
		5032
		5033
		5034
25	Male-sterile AG <i>Rosa hybrida</i> Gly22Term GGA-TGA	5035
		5036
		5037
		5038
		5039
25	Male-sterile AG <i>Rosa hybrida</i> Gly22Term GGA-TGA	5040
		5041
		5042
		5043
		5044

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Male-sterile AG <i>Rosa hybrida</i> Lys23Term AAG-TAG	TATGAAAACAAACCCAACACGGCTCTGGACGCTGATGCCAAAGA AGATTGGAAAGGGATAGATCGAGATCAAGCGGATCGAAAACAC CACCAATCGTCAAGTCACCTCTGCAAAAGGC	5045
	GCCTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTCGATCC GCTTGATCTCGATCTAATCCCCTCCCAATCTCTTGGGCATCAGC GTCCAGGACCGTGTGGTTGGTTCTATA	5046
	GAAGGGGATAGATCGAG	5047
	CTCGATCTAATCCCCTTC	5048
	ACAAACCCAACACGGCTCTGGACGCTGATGCCAAAGAAGATTG GGAAGGGAAAGATCTAGATCAAGCGGATCGAAAACACCACCAAT CGTCAAGTCACCTCTGCAAAAGGCGCAATG	5049
10 Male-sterile AG <i>Rosa hybrida</i> Glu25Term GAG-TAG	CATTGCGCCTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTC CGATCCGCTTGATCTAAGATCTTCCCCTCCCAATCTCTTGGC ATCAGCGTCCAGGACCGTGTGGTTGGTTGG	5050
	GAAAGATCTAGATCAAG	5051
	CTTGATCTAAGATCTTC	5052
	CCAAACACGGCTCTGGACGCTGATGCCAAAGAAGATTGGAAAG GGGAAAGATCGAGATCTAGCGGATCGAAAACACCACCAATCGTCA AGTCACCTCTGCAAAAGGCGCAATGGTTGC	5053
	GCAAACCATTGCGCCTTTGCAGAAGGTGACTTGACGATTGGTGG TGTTTCGATCCGCTAAGATCTCGATCTTCCCCTCCCAATCTCT TTGGGCATCAGCGTCCAGGACCGTGTGG	5054
15 Male-sterile AG <i>Rosa hybrida</i> Lys27 AAG-TAG	TCGAGATCTAGCGGATC	5055
	GATCCGCTAAGATCTCGA	5056
	CAATTGCCGTTCATTTCTTTGACTAAGTAGAAATGGC GTCTCTAAGCGATTATCGACCGAGGTATCGCCCGAGAGGAAAT CGGGAGAGGAAAGATCGAGATCAAACGGA	5057
	TCCGTTGATCTCGATCTTCCCTCCCGATTTCTCTGGCGA TACCTCGGTCGATTATCGCTTAGAGACGCCATTCTACTTAGTCA AAAAGAAAAAAATAAAACAGGCAATTG	5058
	TAAGCGATTATCGACC	5059
20 Male-sterile far <i>Antirrhinum majus</i> Gln7Term CAA-TAA	GGTCGATTATCGCTTA	5060
	GTTTTATTTTCTTTGACTAAGTAGAAATGGCGCTCTAAG CGATCAATCGACCTAGGTATCGCCCGAGAGGAAATCGGGAGAG GAAAGATCGAGATCAAACGGATCGAAAACA	5061
	TGTTTCGATCCGTTGATCTCGATCTTCCCTCCCGATTTCT CTCGGGCGATACCTAGGTGATTGATCGCTTAGAGACGCCATT TACTTAGTCAAAAGAAAAAAATAAAAC	5062
	AATCGACCTAGGTATCG	5063
	CGATACCTAGGTGATT	5064

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile far <i>Antirrhinum majus</i> Glu14Term GAG-TAG	TTTCTTTTGACTAAGTAGAAATGGCGTCTAAGCGATCAATCGA CCGAGGTATGCCCTAGAGGAAATCGGGAGAGGAAAGATCGAG ATCAAACGGATCGAAAACAAACAAATCAAC	5065
		GTTGATTTGTTGTTGATCCGTTGATCTGATCTTCTCTC CCGATTTCTCTA <u>AGGGCGATA</u> CTCGGTCGATTGATCGCTTAGA GACGCCATTCTACTTAGTCAAAAGAAA	5066
		TATGCCCT <u>AGAGGAA</u>	5067
		TTTCTCT <u>AGGGCGATA</u>	5068
10	Male-sterile far <i>Antirrhinum majus</i> Lys16Term AAA-TAA	TTTGACTAAGTAGAAATGGCGTCTAAGCGATCAATCGACCGAG GTATGCCCGAGAGGTAAATCGGGAGAGGAAAGATCGAGATCAA ACGGATCGAAAACAAACAAATCAACAGGTAA	5069
		TAACCTGTTGATTTGTTGTTGATCCGTTGATCTGATCTT CCTCTCCCGATTT <u>ACCTCTCGGGCGATA</u> CTCGGTCGATTGATCG CTTAGAGACGCCATTCTACTTAGTCAAA	5070
		CCGAGAGGTAAATCGGG	5071
		CCCGATT <u>ACCTCTCGG</u>	5072
		TGTCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGA AGGAAAGGGTAAGT <u>AGCAAATAAAGGGGATGTTCCAGAA</u> ATCAAGA AGAGAAGATGTCAGACTCGCCTCAGAGGAA	5073
15	Male-sterile AG <i>Cucumis sativus</i> Leu21Term TTG-TAG	TTCCTCTGAGGCAGGTCTGACATCTCTCTGATTCTGGAAACA TCCCCTTATTGCTACTTACCCCTTCTCTCTTAATCATTCTT GTGAGTGGTGA <u>CTGATAATGCTTGGACA</u>	5074
		GGGTAAGT <u>AGCAAATAA</u>	5075
		TTATTGCT <u>ACTTACCC</u>	5076
		TCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAG GAAAGGGTAAGT <u>GTAAATAAAGGGGATGTTCCAGAA</u> ATCAAGAAG AGAAGATGTCAGACTCGCCTCAGAGGAA	5077
		TCTTCCTCTGAGGCAGGTCTGACATCTCTCTGATTCTGGAA CATCCCCTTATT <u>ACAAC</u> TTACCCCTTCTCTCTTAATCATTCT TTGTGAGTGGTGA <u>CTGATAATGCTTGGACA</u>	5078
20	Male-sterile AG <i>Cucumis sativus</i> Gln22Term CAA-TAA	GTAAGTTG <u>TAATAAAG</u>	5079
		CTTTATT <u>ACAAC</u> TTAC	5080
		CATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAG GGTAAGTTG <u>CAAATAAAGGGGATGTTCCAGAA</u> ATCAAGAAGAGAAG ATGTCAGACTCGCCTCAGAGGAAAGATGGGAA	5081
		TTCCCACCTCTGAGGCAGGTCTGACATCTCTCTGATT CTGGAACATCCCCT <u>ATATTGCAACTTACCC</u> TTCTTCTCCTTA ATCATTCTGTGAGTGGTGA <u>CTGATAATG</u>	5082
		TGCAAAT <u>ATAAGGGGATG</u>	5083
25	Male-sterile AG <i>Cucumis sativus</i> Lys24Term AAG-TAG	CATCCCCT <u>ATATTGCA</u>	5084

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile AG <i>Cucumis sativus</i> Gln28Term CAG-TAG	CCACTCACAGAAATGATTAAGGAAGAAGGAAAGGGTAAGTGCAA ATAAAGGGATGTT <u>T</u> AGAATCAAGAAGAGAAGATGTCAGACTCG CCTCAGAGGAAGATGGAGAGGAAAGATTG	5085
		CAATCTTCTCTCCATCTCCTCTGAGGCGAGTCTGACATCTT CTCTTCTT <u>G</u> ATT <u>T</u> AGAACATCCCCTTATTTGCAACTTACCCCTTC	5086
		GGATGTT <u>T</u> AGAACATCAA	5087
		TTGATT <u>T</u> AGAACATCC	5088
10	Male-sterile AG <i>Zea mays</i> Cys10Term TGC-TGA	CCACCACCACCACCAACCACACCACACCATGCTAACATGAT GA <u>T</u> CTGAGCTGAGCTG <u>A</u> GGGCCGTCGTCCAAGGTCAAGGAGCAGG TGGCGGGCGCGCCGACGGGCTCCGGCGACAGG	5089
		CCTGTCGCCGGAGCCC <u>G</u> TGGCGCCGCCACCTGCTCCTG ACCTTGGACGACGGCC <u>T</u> CAGCTCAGATCAGTCATCATGTTGAGC ATGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	5090
		CTGAGCTG <u>A</u> GGGCCGTC	5091
		GACGGCC <u>T</u> CAGCTCAG	5092
		ACCACCACCACCAACCACACCACACCACACCATGCTAACATGATGACTGATC TGAGCTGCC <u>T</u> GGCCG <u>T</u> AGTCCAAGGTCAAGGAGCAGGTGGCGC GGCGCCGACGGGCTCCGGCGACAGGCAGGGCA	5093
15	Male-sterile AG <i>Zea mays</i> Ser13Term TCG-TAG	TGCCCCTGCCTGTGCCGGAGCCC <u>G</u> TGGCGCCGCCACCT GCTCCTGACCTTGGACTACGGCCCGCAGCTCAGATCAGTCATCA TGGTGGACATGGTGTGGTGGTGGTGGTGGTGGTGGT	5094
		CGGGCCG <u>T</u> AGTCCAAGG	5095
		CCTTGGACTACGGCCCG	5096
		CACCACCACCAACCACACCATGCTAACATGATGACTGATCTGAGC TGCGGGCCGTCG <u>T</u> CTAGGTCAAGGAGCAGGTGGCGCGCGC CGACGGGCTCCGGCGACAGGCAGGGCAGGGCA	5097
		TCCCCTGCCCTGCCTGTGCCGGAGCCC <u>G</u> TGGCGCCGCCGC CACCTGCTCCTGACCT <u>T</u> AGGACGACGGCCCGCAGCTCAGATCAG TCATCATGTTGAGCATGGTGTGGTGGTGGTGGT	5098
20	Male-sterile AG <i>Zea mays</i> Lys15Term AAG-TAG	CGTCGTCC <u>T</u> AGGTCAAG CTTGACCT <u>T</u> AGGACGACG	5099 5100
		CACCACCACCAACCACACCACACCACACCATGCTAACATGATGACTGATCTGAGCTGCCGG CCGTCGTCAAGGT <u>T</u> AGGAGCAGGTGGCGCGCCGACGG GCTCCGGCGACAGGCAGGGCAGGGCAGGGAGAGGCA	5101
		TGCCTCTCCCTGCCCTGCCTGTGCCGGAGCCC <u>G</u> TGGCGC CGCCGCCACCTGCT <u>T</u> AGACCTTGGACGACGGCCCGCAGCTCA GATCAGTCATCATGTTGAGCATGGTGTGGTGGT	5102
		CCAAGGT <u>T</u> AGGAGCAG	5103
		CTGCTCCT <u>T</u> AGACCTTGG	5104
25	Male-sterile AG <i>Zea mays</i> Lys17Term AAG-TAG		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile AG <i>Zea mays</i> Arg4Term CGA-TGA	TCCTACCTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACA AGAGCATGCACATC <del>T</del> GAGAAGAGGAGGCTACACCATCCACAGTAA CAGGCATCATGTCGACCCCTGACTTCGGCGG	5105
		CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGT GTAGCCTCCTCTTCTC <del>A</del> GATGTGCATGCTCTGTTCTATCACACA GATTTGAGGTCTGAAGGAGAAAAGGTAGGA	5106
		TGCACATC <del>T</del> GAGAAGAG	5107
		CTCTCTC <del>A</del> GATGTGCA	5108
10	Male-sterile AG <i>Zea mays</i> Glu5Term GAA-TAA	TACCTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGA GCATGCACATCCGATAAGAGGAGGCTACACCATCCACAGTAACAG GCATCATGTCGACCCCTGACTTCGGCGGGGC	5109
		GCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGAT GGTAGCCTCCTCTT <del>A</del> TCGGATGTGCATGCTCTGTTCTATCA CACAGATTTGAGGTCTGAAGGAGAAAAGGTAA	5110
		ACATCCGATAAGAGGAG	5111
		CTCCTCTT <del>A</del> TCGGATGT	5112
		CTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCA TGCACATCCGAGAA <del>T</del> AGGAGGCTACACCATCCACAGTAACAGGCA TCATGTCGACCCCTGACTTCGGCGGGGCAGC	5113
15	Male-sterile AG <i>Zea mays</i> Glu6Term GAG-TAG	GCTGCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTG GATGGTAGCCTCTT <del>A</del> TCGGATGTGCATGCTCTGTTCTA TCACACAGATTTGAGGTCTGAAGGAGAAAAG	5114
		TCCGAGAA <del>T</del> AGGAGGCT	5115
		AGCCTCCT <del>A</del> TTCTCGGA	5116
		TTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATGC ACATCCGAGAAAGAGTAGGCTACACCATCCACAGTAACAGGCA TGTGACCCCTGACTTCGGCGGGGCAGCAGA	5117
		TCTGCTGCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACT GTGGATGGTAGCCT <del>A</del> CTCTCTCGGATGTGCATGCTCTGTT CTATCACACAGATTTGAGGTCTGAAGGAGAA	5118
20	Male-sterile AG <i>Zea mays</i> Glu7Term GAG-TAG	GAGAAGAGTAGGCTACA	5119
		TGTAGCCT <del>A</del> CTCTTCTC	5120
		GCTGGGTCAAGATCGTGGCGGGCGGTGGCGGGGGAGCAGC GAGAAGATGGGGAGGGGG <del>T</del> AGATCGAGATAAAGCGGATCGAGAA CACGACGAACCGGGCAGGTGACCTCTGCAAGCGCC	5121
		GGCGCTTGCAGAAGGTACACCTGCCGGTCTCGTGTCTCGATC CGCTTATCTCGATCT <del>A</del> CCCCCTCCCCATCTCTCGCTGCTCCCC GCCGCCACCGCCGCCGACGATCCTGACCCAGC	5122
		GGAGGGGGTAGATCGAG	5123
25	Male-sterile AG <i>Oryza sativa</i> Lys5Term AAG-TAG	CTCGATCT <del>A</del> CCCCCTCC	5124

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile AG <i>Oryza sativa</i> Glu7Term GAG-TAG	TCAGGATCGTCGGCGGCGGTGGCGGCGGGAGCAGCGAGAAGA TGGGGAGGGGGAGATCTAGATAAAGCGGATCGAGAACACGACG AACCAGGCAAGGTGACCTTCTGCAAGCGCCGCAATG	5125
		CATTGCGGGCGCTTGAGAAGGTACACCTGCCGGTCGTGTT TCGATCCGCTTATCTAGATCTCCCCCTCCCCATCTTCGCTG CTCCCCGCCACCGCCGACGATCCTGA	5126
		GGAAGATCTAGATAAAG	5127
		CTTATCTAGATCTCC	5128
10	Male-sterile AG <i>Oryza sativa</i> Lys9Term AAG-TAG	TCGTCGGCGGCGGTGGCGGCGGGAGCAGCGAGAAGATGGGG AGGGGGAAAGATCGAGATATAGCGGATCGAGAACACGACGAACCG GCAGGGTACCTTCTGCAAGCGCCGCAATGGCCTC	5129
		GGAGGCCATTGCGGGCGCTTGAGAAGGTACACCTGCCGGTCGT GTGTTCTCGATCCGCTATATCTCGATCTCCCCCTCCCCATCTTCT CGCTGCTCCCGCCACCGCCGACGA	5130
		TCGAGATATAGCGGATC	5131
		GATCCGCTATATCTCGA	5132
		GCGGTGGCGGCGGGAGCAGCGAGAAGATGGGGAGGGGGAG ATCGAGATAAAGCGGATCTAGAACACGACGAACCGGCAGGTGAC CTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG	5133
15	Male-sterile AG <i>Oryza sativa</i> Glu12Term GAG-TAG	CCTCTTCAGGAGGCCATTGCGGCCTTGAGAAGGTACACCTGC CGGTTCGTCGTGTTCTAGATCCGCTTATCTCGATCTCCCCCTC CCCATCTCTCGCTGCTCCCCGCCACCGC	5134
		AGCGGATCTAGAACACG	5135
		CGTGTCTAGATCCGCT	5136

Table 16  
Oligonucleotides to produce male-sterile plants

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
20	Male-sterile PI <i>Cucumis sativus</i> Tyr21Term TAT-TAG	GGGAAGAGGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAAT AGACAAGTTACATAGTCAGAGAGAAATGGTATCATCAAAAAAG CCAAAGAAATTACTGTTCTTGCATGCT	5137
		AGCATCGCAAAGAACAGTAATTCTTGGCTTTTGATGATACCAT TTCTTCTCTTGAATGTAACTTGCTATTGCTTGAGTTCTATTG TTTTATTTCTATTCCCTCTTCCC	5138

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTACATA <u>G</u> CAAAGAG	5139
	CTCTTT <u>G</u> ACTATGTAAC	5140
5 Male-sterile PI <i>Cucumis sativus</i> Ser22Term TCA-TGA	GAAGAGGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAATAG ACAAGTTACATATT <u>G</u> AAAGAGAAGAAATGGTATCATCAAAAAAGCC AAAGAAATTACTGTTCTTGCATGCTCA TGAGCATCGAAAGAACAGTAATTCTTGGCTTTTGATGATACC ATTTCTTCTTT <u>C</u> AAATATGTAACTTGTCTATTGCTTGAGTTCTAT TCTTTTATTCTATTCCCTCTC TACATATT <u>G</u> AAAGAGAA	5141 5142 5143 5144
10 Male-sterile PI <i>Cucumis sativus</i> Lys23Term AAG-TAG	AGAGGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAATAGAC AAGTTACATATT <u>C</u> ATAGAGAAGAAATGGTATCATCAAAAAAGCCAAA GAAATTACTGTTCTTGCATGCTCAAG CTTGAGCATCGAAAGAACAGTAATTCTTGGCTTTTGATGATA CCATTCTCT <u>C</u> ATGAATATGTAACTTGTCTATTGCTTGAGTTCTC TATTCTTTTATTCTATTCCCTCT CATATT <u>C</u> ATAGAGAAGA	5145 5146 5147 5148
15 Male-sterile PI <i>Cucumis sativus</i> Arg24Term AGA-TGA	GGGAAAATAGAAATAAAAGAATAGAGAACTCAAGCAATAGACAAG TTACATATT <u>C</u> AAAG <u>T</u> GAAGAAATGGTATCATCAAAAAAGCCAAAGAA ATTACTGTTCTTGCATGCTCAAGTT AAACTTGAGCATCGAAAGAACAGTAATTCTTGGCTTTTGATG ATACCATTCTTC <u>ACT</u> TTGAATATGTAACTTGTCTATTGCTTGAGTT CTCTATTCTTTTATTCTATTCC ATTCAA <u>AGT</u> GAAGAAAT	5149 5150 5151 5152
20 Male-sterile PI <i>Malus domestica</i> Tyr21Term TAC-TAG	GGGACGTGGGAAGGGTGAGATCAAGAGGATTGAGAACTCAAGTAA CAGGCAGGTGACCTAG <u>T</u> CCAAGAGGAGGAATGGGATTATCAAGAA GGCAAAGGAGATCACTGTTCTATGTGATGCT AGCATCACATAGAACAGTGATCCCTTGCCTTCTTGATAATCCCA TTCCCTCCTTGGACT <u>AG</u> GTCA <u>C</u> CTGCCTGTTACTTGAGTTCTCAA TCCTCTTGATCTCAACCTCCCACGTCCC GTGACCT <u>AGT</u> CCAAGAG	5153 5154 5155 5156

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Male-sterile PI <i>Malus domestica</i> Lys23Term AAG-TAG	CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGG CAGGTGACCTACTCCTAGAGGGAGGAATGGGATTATCAAGAAGGCA AAGGAGATCACTGTTATGTGATGCTAAAG	5157
	CTTAGCATCACATAGAACAGTGATCTCCTTGCCCTTGTATAATC CCATTCCCTCTAGAGTAGGTCACCTGCCTGTTACTTGAGTTCT	5158
	CAATCCTCTGATCTCACACCTCCCACG	
	CCTACTCCTAGAGGAGG	5159
10 Male-sterile PI <i>Malus domestica</i> Lys30Term AAG-TAG	CCTCCTCTAGAGGAGTAGG	5160
	AGGATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGG AGGAATGGGATTATCTAGAACAGGAAAGGAGATCACTGTTATGTG	5161
	ATGCTAAAGTATCTCTTATCATTATTCTA	
	TAGAATAAAATGATAAGAGATACTTAGCATCACATAGAACAGTGATC TCCTTGCCTCTAGATAATCCCATTCCCTCTGGAGTAGGTCA	5162
	CCTGCCTGTTACTTGAGTTCTCAATCCT GGATTATCTAGAACAGGCA	5163
15 Male-sterile PI <i>Malus domestica</i> Lys31Term AAG-TAG	TGCCTCTAGATAATCC	5164
	ATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGG AATGGGATTATCAAGTAGGCAAAGGAGATCACTGTTATGTGATG	5165
	CTAAAGTATCTCTTATCATTATTCTAGCT	
	AGCTAGAATAAAATGATAAGAGATACTTAGCATCACATAGAACAGT GATCTCCTTGCCTACTTGATAATCCCATTCCCTCTGGAGTAG	5166
	GTCACCTGCCTGTTACTTGAGTTCTCAAT TTATCAAGTAGGCAAAG	5167
20 Male-sterile globosa <i>Antirrhinum majus</i> Gly2Term GGA-TGA	CTTTGCCTACTTGATAAA	5168
	CATTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAA AAACAAAAAAATGTGAAGAGGAAAATTGAGATCAAAGAATTGAG	5169
	AACTCAAGCAACAGGCAGGTTACTTACT	
	AGTAAGTAACCTGCCTGTTGCTGAGTTCTCAATTCTTTGATCTCA ATTTTCTCTTCACATTTTTGTTTTGTTCTCTCTGTTTG	5170
	TTTGCAGATAACTATTGAAAAATG AAAAAATGTGAAGAGGA	5171
25 Male-sterile globosa <i>Antirrhinum majus</i> Arg3Term AGA-TGA	TCCTCTTCACATTTTT	5172
	TTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAA CAAAAAAAATGGGATGAGGAAAATTGAGATCAAAGAATTGAGAAC	5173
	TCAAGCAACAGGCAGGTTACTTACTCAA	
	TTGAGTAAGTAACCTGCCTGTTGCTGAGTTCTCAATTCTTTGATC TCAATTCTCTCATCCCATTTTTGTTTTGTTCTCTCTGTT TTGTTGCAGATAACTATTGAAAA	5174

	Phenotype: Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile globosa <i>Antirrhinum majus</i> Gly4Term GGA-TGA	AAATGGGAT <u>GAGGAAAA</u>	5175
		TTTCCTCAT <u>CCCATTT</u>	5176
		TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAA AAAAATGGGAAGAT <u>GAAAAATTGAGATCAAAGAATTGAGAACTCA</u> AGCAACAGGCAGGTTACTTACTCAAAGA	5177
		TCTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTG ATCTCAATT <u>TTTCACTTCCCATTTTTGTTTTGTTTTCTCTTT</u> GTTTTGTTGCAGATAACTATTGTA	5178
		TGGGAAGAT <u>GAAAAATT</u>	5179
		AATTTTC <u>ATCTTCCC</u> A	5180
	Male-sterile globosa <i>Antirrhinum majus</i> Lys5Term AAA-TAA	AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAAA AATGGGAAGAGG <u>ATAAAATTGAGATCAAAGAATTGAGAACTCAAGC</u> AACAGGCAGGTTACTTACTCAAAGAGAA	5181
		TTCTCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTT TTGATCTCAATT <u>ATCCTCTCCCATTTTTGTTTTGTTTTCTCT</u> CTTGTGTTGTTGCAGATAACTATT	5182
		GAAGAGG <u>ATAAAATTGAG</u>	5183
		CTCAATT <u>ATCCTCTTC</u>	5184
		GCTGAGCTCTGCTGCCCTGGATCTGTTGGAGTGGAGAACGCAGTATG AGTATGGGGCGCGG <u>CTAGATCAAGATCAAGAGGATCGAGAACTCT</u> ACCAACC <u>GGCAGGTGACCTCTCCAGCGCC</u>	5185
15	Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	GGCGCTTGAGAAGGT <u>CACCTGCCGGTTGGTAGAGTTCTCGATCC</u> TCTTGATCTGAT <u>CTAGCCGCGCCCCATACTGCGTTCTCCACTCC</u> CAAACAGAT <u>CCAAGGGCAGCAAGAGCTCAGC</u>	5186
		GGCGCGG <u>CTAGATCAAG</u>	5187
		CTTGAT <u>CTAGCCGCGCC</u>	5188
		CTCTTGCTGCCCTGGATCTGTTGGAGTGGAGAACGCAGTATG GGGCGCGG <u>CAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC</u> CGGCAGGT <u>GACCTCTCCAGCGCCGGCCG</u>	5189
		CGGCCCGGCG <u>CTGGAGAAGGTACCTGCCGGTTGGTAGAGTT</u> TCGAT <u>CCCTTGATCTAGATCTGCCGCGCCCCATACTGCGTTCTC</u> CACT <u>CCCAAACAGATCCAAGGGCAGCAAGAG</u>	5190
20	Male-sterile PI <i>Zea mays</i> Lys7Term AAG-TAG	GCAAGAT <u>CTAGATCAAG</u>	5191
		CTTGAT <u>CTAGATCTTG</u> C	5192

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTGGAGTGGAGAACGGAGTATG GGGCGCGGCAAGAT <u>CT</u> AGATCAAGAGGGATCGAGAACCTACCAAC CGGCAGGTGACCTTCCAAGCGCCGGCCG	5193
		CGGCCCGGCGCTTGGAGAAGGTACACCTGCCGGTTGGTAGAGTTC TCGATCCTTGTAT <u>CT</u> AGATCTTGCAGCCCCATACTGCGTTCTC CACTCCAAACAGATCCAAGGGCAGCAAGAG	5194
		GCAAGAT <u>CT</u> AGATCAAG	5195
		CTTGAT <u>CT</u> AGATCTTGC	5196
10	Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	GATCTGTTGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGAT CAAGATCAAGAGGGAT <u>CT</u> AGAACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGGCGACTGGTCAAGAAGG	5197
		CCTTCTTGACCAGTCGGCCCGGCGCTTGGAGAAGGTACCTGC CGGTTGGTAGAGTT <u>CT</u> AGATCCTTGTATCTTGATCTTGCAGCGC CCCATACTGCGTTCTCCACTCCAAACAGATC	5198
		AGAGGAT <u>CT</u> AGAACTCT	5199
		AGAGTT <u>CT</u> AGATCCTCT	5200
		GCTGAGCTTGCTGCCCTGAATCTGTTAGGGAGTGGAGAACGG AGTATGGGGCGCGG <u>CT</u> AGATCGAGATCAAGAGGGATCGAGAACCT ACCAACCGGCAGGTGACCTTCCAAGCGCC	5201
15	Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	GGCGCTTGGAGAAGGTACCTGCCGGTTGGTAGAGTTCTCGATCC TCTTGATCTCGAT <u>CT</u> AGCCCGCCCCATACTCCGTTCTCCACTCC CTAACAGATTCAAGGGCAGCAAGAGCTCAGC	5202
		GGCGCGG <u>CT</u> AGATCGAG	5203
		CTCGAT <u>CT</u> AGCCCGGCC	5204
		CTCTTGCTGCCCTGAATCTGTTAGGGAGTGGAGAACGGAGTATG GGGCGCGGCAAGAT <u>CT</u> AGATCAAGAGGGATCGAGAACCTACCAAC CGGCAGGTGACCTTCCAAGCGCCGGCCG	5205
		CGGCCCGGCGCTTGGAGAAGGTACACCTGCCGGTTGGTAGAGTTC TCGATCCTTGTAT <u>CT</u> AGATCTTGCAGCCCCATACTCCGTTCTC CACTCCCTAACAGATTCAAGGGCAGCAAGAG	5206
20	Male-sterile PI <i>Zea mays</i> Glu7Term GAG-TAG	GCAAGAT <u>CT</u> AGATCAAG	5207
		CTTGAT <u>CT</u> AGATCTTGC	5208
		CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCG CGGCAAGATCGAGAT <u>CT</u> AGAGGGATCGAGAACCTACCAACCGGCA GGTGACCTTCCAAGCGCCGGCCGGACTGG	5209
		CCAGTCCGGCCCGGCGCTTGGAGAAGGTACACCTGCCGGTTGGTA GAGTTCTCGATCCT <u>CT</u> AGATCTCGATCTTGCAGCCCCATACTC CGTTCTCCACTCCCTAACAGATTCAAGGGCAG	5210

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	TCGAGATCTAGAGGATC	5211
		GATCCTCTAGATCTGA	5212
		AATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGAT CGAGATCAAGAGGATCTAGAACTCTACCAACCAGGCAAGGTGACCTT CTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	5213
		CCTCTTGACCAGTCGGCCGGCGCTTGGAGAAAGGTACACCTGC CGGTTGGTAGAGTTCTAGATCCTCTTGATCTGATCTGCCGCGC CCCATACTCCGTTCTCACTCCCTAACAGATT	5214
		AGAGGATCTAGAACTCT	5215
		AGAGTTCTAGATCCTCT	5216
	Male-sterile PI <i>Oryza sativa</i> Lys5Term AAG-TAG	TTGCTGCTAAGCTAGCTGGAGGAAGGGAGGAGGAGGAGGAGGAGG CGGGATGGGGCGCGGGTAGATCGAGATCAAGAGGATCGAGAACT CCACCAACCGCCAGGTGACCTCTCCAAGCGCA	5217
		TGCGCTTGGAGAAAGGTACCTGGCGTTGGTGGAGTTCTCGATCC TCTTGATCTGATCTACCCCGCCCCATCCGCCTCCCTCCCTC CTCCTCCTCCCTCCAGCTAGCTTAGCAGCAA	5218
		GGCGCGGGTAGATCGAG	5219
		CTCGATCTACCCCGCC	5220
		CTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGG TGGGGCGCGGGAAAGATCTAGATCAAGAGGATCGAGAACTCCACC AACCGCCAGGTGACCTCTCCAAGCGCAGGAGCG	5221
10	Male-sterile PI <i>Oryza sativa</i> Glu7Term GAG-TAG	CGCTCCTGCGCTTGGAGAAAGGTACCTGGCGTTGGAGTT TCGATCCTTGTAGATCTCCCGCCCCATCCGCCTCC CCTCCTCCTCCCTCCAGCTAGCTTAG	5222
		GGAAGATCTAGATCAAG	5223
		CTTGATCTAGATCTCC	5224
		TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG GCGGGAAAGATCGAGATCTAGAGGATCGAGAACTCCACCAACCGC CAGGTGACCTCTCCAAGCGCAGGAGCGGGATCC	5225
		GGATCCCGCTCCTGCGCTTGGAGAAAGGTACCTGGCGTTGGT GAGTTCTGATCCTCTAGATCTGATCTCCCGCCCCATCCCG CCTCCTCCTCCCTCCCTCCAGCTA	5226
15	Male-sterile PI <i>Oryza sativa</i> Lys9Term AAG-TAG	TCGAGATCTAGAGGATC	5227
		GATCCTCTAGATCTGA	5228

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI <i>Oryza sativa</i>	GAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAAGA TCGAGATCAAGAGGGATCT <u>AGA</u> ACTCCACCAACCGCCAGGTGACCT TCTCCAAGCGCAGGAGCGGGATCCTCAAGAAGG	5229
Glu12Term GAG-TAG	CCTTCTTGAGGATCCCGCTCCTGCGCTTGGAGAAGGTACCTGGC GGTTGGTGGAGTTCTAGATCCTTTGATCTCGATCTCCCGGCC CCATCCCGCCTCCTCCTCCTCCTCCTTC	5230
	AGAGGATCT <u>AGA</u> ACTCC	5231
	GGAGTTCT <u>AG</u> ATCCTCT	5232

**Example 7**  
**Engineering plants for abiotic stress tolerance**

Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy metals, and extreme temperature, are major factors limiting plant growth and productivity. The 5 worldwide loss in yield of three major cereal crops, rice, maize, and wheat due to water stress (drought) has been estimated to be over ten billion dollars annually and many currently marginal soils could be brought into cultivation if suitable plant varieties were available.

Physiological and biochemical responses to high levels of ionic or nonionic solutes and decreased water potential have been studied in a variety of plants. It is known, for example, that increasing 10 levels of alcohol dehydrogenase can confer enhanced flooding resistance in plants. There are also several possible mechanisms to enhance plant salt tolerance. For example, one mechanism underlying the adaptation or tolerance of plants to osmotic stresses is the accumulation of compatible, low molecular weight osmolytes such as sugar alcohols, special amino acids, and glycinebetaine. Such accumulation can be engineered, for example, by removing feedback inhibition on 1-pyrroline-t-carboxylate synthetase, which 15 results in accumulation of proline. Additionally, recent experiments suggest that altering the expression or activity of specific sodium or potassium transporters can confer enhanced salt tolerance.

Plant tolerance of contamination by heavy metals such as lead and aluminum in soils has also been investigated and one mechanism underlying tolerance is the production of dicarboxylic acids such as oxalate and citrate. In addition, individual genes involved in heavy metal sensitivity have been identified.

20 The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer stress tolerance in plants.

**Table 17**  
**Genome-Altering Oligos Conferring Stress Tolerance**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Salt Tolerance P5CS <i>Arabidopsis thaliana</i> Phe128Ala TTT-GCT	CGTCTTTGTGTGGTAGTGGATGTGACGGTTGCTCAAATGCTT GTGACCGATAGCAGTGCTAGAGATAAGGATTCAGGAAGCAACTT AGTGAAACTGTCAAAGCGATGCTGAGGATGA	5233
		TCATCCTCAGCATCGCTTGACAGTTCACTAAGTTGCTTCCTGAA ATCCTTATCTCT <u>AGC</u> ACTGCTATCGGTACAAGCATTGAGCAACC GTCACATCCAACCTACCACACAAAAAGACG	5234
		ATAGCAGTG <u>C</u> TAGAGAT	5235
		ATCTCT <u>G</u> ACTGCTAT	5236
10	Salt Tolerance P5CS 1 <i>Brassica napus</i> Phe128Ala TTC-GCC	GAGACTATGTTGACCAGCTGGATGTGACGGTGCTCAGCTGCTG GTGAATGACAGTAGT <u>G</u> CCAGAGACAAGGAGTTAGGAAGCAACTT AATGAGACAGTGAAGTCCATGCTTGATTGA	5237
		TCAAATCAAGCATGGACTTCACTGTCTCATTAAGTTGCTTCCTGAA CTCCTTGTCTCT <u>GGC</u> ACTACTGTCATTCAACCAGCAGCTGAGCAGC CGTCACATCCAGCTGGTCAAACATAGTCTC	5238
		ACAGTAGTG <u>C</u> CAGAGAC	5239
		GTCTCT <u>GGC</u> ACTACTGT	5240
		GAGACTATGTTGACCAGATGGATGTGACGGTGCTCAAATGCTG GTGACTGATAGCAGTG <u>C</u> TAGAGATAAGGATTCAGGAAGCAACTT AGTGAGACAGTCAAAGCTATGCTGAAATGA	5241
15	Salt Tolerance P5CS 2 <i>Brassica napus</i> Phe129Ala TTC-GCC	TCATTTCAGCATAGCTTGACTGTCTCACTAAGTTGCTTCCTGAA ATCCTTATCTCT <u>GAC</u> ACTGCTATCAGTCACCAGCATTGAGCCACC GTCACATCCATCTGGTCAAACATAGTCTC	5242
		ATAGCAGTG <u>C</u> TAGAGAT	5243
		ATCTCT <u>G</u> ACTGCTAT	5244
		GATATGTTGTTAACCAACTGGATGTCTCGTCATCTCAACTTCTG TCACCGACAGTGAT <u>G</u> CTGAGAACCCAAAGTTCCGGGAGCAACTCA CTGAAACTGTTGAGTCATTATTAGATCTTA	5245
20	Salt Tolerance P5CS <i>Oryza sativa</i> Phe128Ala TTT-GCT	TAAGATCTAATAATGACTAACAGTTCACTGAGTTGCTCCGGAA CTTGGGTTCT <u>CAG</u> CATCACTGTCGGTGACAAGAAGTTGAGATGA CGAGACATCCAGTTGGTAAACAAACATATC	5246
		ACAGTGAT <u>G</u> CTGAGAAC	5247
		GTTC <u>T</u> CAGCATCACTGT	5248

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Salt Tolerance P5CS <i>Medicago sativa</i> Phe128Ala TTT-GCT	GATATTTGTTAGTCAGCTGGATGTGACATCTGCTCAGCTTCTG TTACTGACAATGAT <u>GCT</u> AGAGACCAAGATTTAGAAAGCAACTTC TGAAACTGTGAGATCACTTCTAGCACTAA	5249
		TTAGTGCTAGAAGTGTCTCACAGTTCAAGAAAGTTGCTTCTAA ATCTGGTCTCTAG <u>GCT</u> ATTGTCAGTAACAAGAAGCTGAGCAGAT GTCACATCCAGCTGACTAAACAAAATATC	5250
		ACAATGAT <u>GCT</u> AGAGAC	5251
		GTCTCTAG <u>GCT</u> ATTGT	5252
10	Salt Tolerance P5CS <i>Actinidia deliciosa</i> Phe128Ala TTT-GCT	GATACATTGTTAGTCAGCTGGATGTGACATCAGCTCAGCTACTC GTTACTGATAATGAT <u>GCT</u> AGGGATCCAGAATTAGGAAGCAACTTA CTGAAACTGTAGAACATCACTATTGAATTG	5253
		TCAAATTCAATAGTGTATTCTACAGTTCAAGTTGCTTCTGAAT TCTGGATCCCTAG <u>GCT</u> ATTATCAGTAACGAGTAGCTGAGCTGAT GTCACATCCAGCTGACTAAACAAATGTATC	5254
		ATAATGAT <u>GCT</u> AGGGAT	5255
		ATCCCTAG <u>GCT</u> ATTAT	5256
		GACACACTCTCAGTCAACTGGATGTGACATCAGCACAGCTTCTT GTAACAGATAATGAC <u>GCC</u> CAGAAGTCCAGAATTAGAAAACAACCTTA CTGAAACAGTCGATTCTTATTATCTTATA	5257
15	Salt Tolerance P5CS <i>Cichorium intybus</i> Phe122Ala TTC-GCC	TATAAGATAATAAAGAACATGACTGTTCAAGTTGTTCTAAAT TCTGGACTCTCTGGCGTCATTATCTGTTACAAGAAGCTGTGCTGAT GTCACATCCAGTTGACTGAAGAGTGTGTC	5258
		ATAATGAC <u>GCC</u> CAGAAGT	5259
		ACTTCTGGCGTCATTAT	5260
		GATTCTTGTTCAGTCAGITGGATGTGACATCAGCTCAGCTTCTGG TGACTGATAATGAC <u>GCT</u> AGAGATCCAGATTTAGGAGACAACCTCAA TGACACAGTAAATTGTTGCTTCTCTAA	5261
20	Salt Tolerance P5CS <i>Lycopersicon esculentum</i> Phe128Ala TTT-GCT	TTAGAGAAAGCAACGAATTACTGTGTCAATTGAGTTGCTCCTAA ATCTGGATCTCTAG <u>GCT</u> ATTATCAGTCACCAGAACGCTGAGCTGA TGTACATCCAACGTGACTGAACAAAGAACATC	5262
		ATAATGAC <u>GCT</u> AGAGAT	5263
		ATCTCTAG <u>GCT</u> ATTAT	5264
		GATACCAGTTCAGCCAGCTTGTGACTTCTCCAACTTCTTG TGAATGATGGATTG <u>GCT</u> AGGGATGCTGGCTTCAGAAAACAACCTTC GGACACAGTGAACCGCGTATTAGATTAA	5265
25	Salt Tolerance P5CS <i>Vigna unguiculata</i> Phe162Ala TTT-GCT	TTAAATCTATAACCGCGTCACTGTGTCCGAAAGTTGTTCTGAA GCCAGCATCCCTAG <u>CAA</u> ATCCATCATTACAAGAACGTTGGGAAGA AGTCACATCAAGCTGGCTGAACATGGTATC	5266
		ATGGATTG <u>GCT</u> AGGGAT	5267

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		ATCCCTAGCAAATCCAT	5268
5	Salt Tolerance P5CS <i>Mesembryanthemum crystallinum</i> Phe125Ala TTT-GCT	GACACCTTGTAGTCAGTGGATCTGACTGCTGCTCAGCTGCTT GTGACGGACAACGAC <u>G</u> CTAGAGATCCAAGTTAGAACACAACTA ACTGAAACAGTGTATCAGTTGGATCTAA	5269
		TTAGATCCAACAACTGATACACTGTTCAGTTAGTTGTGTTCTAAA CTTGGATCTCTAGCGTCGTTGCCGTACAAGCAGCTGAGCAGCA GTCAGATCCAACGTGACTAAACAAGGTGTC	5270
		ACAACGAC <u>G</u> CTAGAGAT	5271
		ATCTCTAGCGTCGTTGT	5272
10	Salt Tolerance P5CS <i>Vitis vinifera</i> Phe130Ala TTT-GCT	GACACATTATTTAGCCAGCTGGATGTGACATCAGCTCAGCTTCTT GTGACTGATAATGAT <u>G</u> CTAGGGATGAAGCTTCCGAAATCAACTTA CTCAAACAGTGGATTCTATTGTTAGCTTGA	5273
		TCAAAGCTAACATGAATCCACTGTTGAGTAAGTTGATTGAA AGCTTCATCCCTAG <u>G</u> CATCATTATCAGTCACAAGAAGCTGAGCTGAT GTCACATCCAGCTGGCTAAATAATGTGTC	5274
		ATAATGAT <u>G</u> CTAGGGAT	5275
		ATCCCTAG <u>G</u> ATCATTAT	5276
15	Salt Tolerance P5CS <i>Vigna aconitifolia</i> Phe129Ala TTT-GCT	GATACGCTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTT GTGACGGATAACGAT <u>G</u> CTCGAGATAAGGATTCAGGAAGCAGCTT ACTGAGACTGTGAAGTCGCTGTTGGCGCTGA	5277
		TCAGCGCCAACAGCGACTTCACAGTCTCAGTAAGCTGCTTCTGA AATCCTTATCTCGAG <u>G</u> ATCGTTATCCGTACAAGAAGCTGAGCCG ATGTCACATCGAGCTGAGTGAACACAGCGTATC	5278
		ATAACGAT <u>G</u> TCGAGAT	5279
		ATCTCGAG <u>G</u> ATCGTTAT	5280
20	Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Ser207Val TCC-GTC	AGAGATGTTCTAGTCCAAGAAATCTCACCTCTCACTTCTCCG TCTTCACAAACAGTT <u>G</u> TCACGTTGCAAACCTGGGATTTGTCCCCAC GAATGAGAACATGATCATCTTCGCAAAA	5281
		TTTGCGAAAGATGATCATGTTCTCATCGTGGGGACAAATCCGCA GTTGCAAACGT <u>G</u> CAACTGTTGTGAAGACGGAGAAAGTGAGAGG TGAGATTCTTGGAACTAAGAACATCTCT	5282
		CAACAGTT <u>G</u> TCACGTT	5283
		AAACGTG <u>G</u> CAACTGTTG	5284
25	Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Gln237Leu CAA-CTA	CGAATGAGAACATGATCATCTTCGCAAAAACCTGGTCTCATCTG GCTCCTAATCCCTCTAGTACTGATGGGAAACACTTGTCCCTGC TTCTGGTTTGCTCATATGGGGACTTTA	5285
		TAAAGTCCCCATATGAGCAAACCAAGAAGCAAGGGAACAAAGTG TTTCCCATCAGTACTAGAGGGATTAGGAGCCAGATGAGACCAGAG TTTTGCGAAAGATGATCATGTTCTCATTG	5286

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCCCTCTAGTACTGA	5287
	TCAGTACTAGAGGGATT	5288
5 Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Asn332Ser AAT-AGT	AGTCTCTAGAAGGAATGAGTCGTACGAGAAGTTGGTGGATCGT TGTTCAAGTGGTGAGTCGCGACACACCGGAGAACTATAGTAG ACCTCTACACTTCCCCAGCTATCTGGT	5289
	ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTCT CCGGTGTGTCGCGA <b>ACT</b> ACCACTGAAACAACGATCCAACCAAC TTCTCGTACGA <b>ACT</b> CTCCCTTAGAGACT	5290
	AGTGGTGAGTCGCGAC	5291
	GTCGCGA <b>ACT</b> ACCACT	5292
10 Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Ser256Val TCG-GTG	AGAGATGTGCTAAAGAAGAAAGGTCTCAAATGGTGACCTTTCC GTCTTCACCACCGTGG <b>TG</b> ACCTTTGCCAGTTGTGGGTTGTCCCG ACCAATGAAA <b>AC</b> TGATTATCTTCAGCAAA	5293
	TTTGCTGAAGATAATCATGTTTCATTGGTCGGGACAAACCCACA ACTGGCAAAGGTCA <b>CC</b> ACCGTGGTGAAGACGGAAAAGGTACCA TTTGAGACCTTTCTCTTTAGCACATCTCT	5294
	CCACCGTGG <b>TG</b> ACCTTT	5295
	AAAGGTCA <b>CC</b> ACCGTGG	5296
15 Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Gln286Leu CAG-CTG	CCAATGAAA <b>AC</b> TGATTATCTTCAGCAAAACTCTGGCCTCCCT GATTCTCATCCCT <b>TG</b> GGCCCTTCTTGGGACATGCTGTTCCC <b>ATC</b> GAGCCTACGTTGACGCTTGG <b>CT</b> CATCGG	5297
	CCGATGAGCCAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT GTTCCAAGAAGGG <b>CC</b> <b>A</b> GAGGGATGAGAATCAGGAGGAGGCCA GAGTTTTGCTGAAGATAATCATGTTTCATTGG	5298
	CATCCCT <b>TG</b> GGCCCTTC	5299
	GAAGGG <b>CC</b> <b>A</b> GAGGGATG	5300
20 Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Asn381Ser AAC-AGC	AATCGTTGAATGGACTAAGCTCCTGTGAGAAAATCGTGGGCCGC TGTTCA <b>GT</b> CGTGA <b>G</b> CAGCAGACATACCGGCAGACGGTCGTC GATCTGTCCACAGTTGCTCCGCCATCTGGT	5301
	ACCAAGATGGGGAGCAACTGTGGACAGATCGACGACC <b>GT</b> CTC GCCGGTATGTCTGCT <b>G</b> CTCACCGACTGAAACAGCGCGCCACGA TTTCTCACAGGAGCTTAGTCCATTCAACGATT	5302
	GTGCGTGAG <b>C</b> AGCAGAC	5303
	GTCTGCT <b>G</b> CTCACGCAC	5304

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Salt Tolerance HKT1 <i>Oryza sativa</i> Ser238Val TCC-GTC	AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTTCAT TCTCGGTACCGTC <u>G</u> TCGTTGCGAATGTGGGGCTCGTGCCG ACAAATGAGAACATGGCAATCTTCTCCAAGA	5305
	TCTTGGAGAAGATTGCCATGTTCTCATTTGTCGGCACGAGCCCCA CATTGCAA <u>ACGAGACG</u> ACCCTGACCGAGAATGAGAACAGTGCA ATGTTGATCCCTTCTTCAGTGGAGCTT	5306
	TCACGGTC <u>G</u> TCTCGTT	5307
	AAACGAGACGACCCTGA	5308
10 Salt Tolerance HKT1 <i>Oryza sativa</i> Gln268Leu CAG-CTG	CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCC TCCTGTTCATCGGCC <u>T</u> GATTCTTGCAAGGCAATACACTTACCCCT CTTCCTAAGGCTATTGATATGGTTCTGGG	5309
	CCCAGGAACCATATCAATAGCCTTAGGAAGAGAGGGTAAAGTGTA TTGCCTGCAAGAACAT <u>CAGGCCGAT</u> GAACAGGAGGAGGAGGCCGG GTTCTGGAGAAGATTGCCATGTTCTCATTG	5310
	CATCGGCC <u>T</u> GATTCTTG	5311
	CAAGAACAT <u>CAGGCCGAT</u> G	5312
	CATGCTTGTGGACTCAGCTTACCAAGAACATTCAATGCATT GTTCATGGCAGTG <u>AGCG</u> CAAGGCACTCGGGGGAGAACTCCATCG ACTGCTCACTCATGCCCTGCTGTTCTAGT	5313
15 Salt Tolerance HKT1 <i>Oryza sativa</i> Asn363Ser AAC-AGC	ACTAGAACAGCAGGGCGATGAGTGAGCAGTCGATGGAGTTCTC CCCCGAGTGCC <u>T</u> CGCTCACTGCCATGAACATGCATTGATAAT CTTCTGGTAAGAGCTGAGTCCATCAAAGACTG	5314
	GGCAGTG <u>AGCG</u> CAAGGC	5315
	GCCTTGCG <u>T</u> CACTGCC	5316
	GTGCCCAACTGAACAAAGAACAGGGATCAACATCGTGC <u>T</u> TCAC TATCAGTCACCGTT <u>G</u> TCCTGCGAATGCAGGACTCGTGCCA CAAATGAGAACATGGCATCTTCTCAAAGAA	5317
	TTCTTGAGAACATGACCATGTTCTCATTTGCGAGTCCT GCATTGCA <u>ACAGGAGAC</u> ACACGGTGACTGATAGTGAGAACAGCAC GATGTTGATCC <u>T</u> CTGTTGAGTGGGCAC	5318
20 Salt Tolerance HKT1 <i>Triticum aestivum</i> Ala240Val GCC-GTC	CACC <u>GGT</u> T <u>G</u> CTCCTGTG CACAGGAG <u>ACAACGGT</u> G	5319
	CACAGGAG <u>ACAACGGT</u> G	5320
	CAAATGAGAACATGGCATCTTCTCAAAGAACATTGAGGCC <u>T</u> GT GCTGCTGAGTG <u>GGC</u> <u>T</u> GATGCTCGCAGGCAATACATTGTTCCCT CTTCCTGAGGCTACTGGTG <u>GGT</u> CTGGTCTGG	5321
	CCCAGGAACCA <u>ACCCAGT</u> AGCCTCAGGAAGAGAGGGAACATGT ATTGCCTGCGAGC <u>ATCAGGCC</u> ACTCAGCAGCAACAGAGGCC <u>T</u> G AATTCTTGAGAACATGACCATGTTCTCATTG	5322
	GAGTGGCC <u>T</u> GATGCTG	5323

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Salt Tolerance HKT1 <i>Triticum aestivum</i> Asn365Ser AAT-AGT	CGAGCATCAGGCCACTC	5324
	CAGTCTTGTATGGGCTCAGCTCTTATCAGAAGACTGTCAATGCATT CTTCATGGTGGTGAGTGCAGGGACTCAGGGGAGAATTCCATCG ACTGCTCGCTCATGTCCCCTGCCATTATAGT	5325
	ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCC CCTGAGTGCGCTCGCACTCACCACCATGAAGAATGCATTGACAGTC TTCTGATAAGAGCTGAGCCCATCAAAGACTG	5326
	GGTGGTGAGTGCAGGGC	5327
	GCCTCGCACTCACCACC	5328
	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg7Term CGA-TGA	5329
10 Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg7Term CGA-TGA	TTTTTTTGTGTTCTGTTCAAAAACAAAATCTTGAATTATGGCA ACCCGTCTTCTCTGAACAAACTTATCCGGCGATCTTACCGTTAC CCGCTTTAGCCCGGTGGGTCCCTCCCA	5330
	TGGGAGGACCCACCGGGCTAAAAGCGGGTAAACGGTAAGATCGC CGGATAAAAGTTGTTCAAGAGAAGACGGGTTGCCATAAAATTCAA GATTTTGTGTTGAAAACGAAAACAAAAAAA	5331
	GTCTTCTCTGAACAAAC	5332
	GTTTGTTCAGAGAAGAC	5333
15 Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg13Term CGA-TGA	TCAAAAACAAAATCTTGAATTATGGCAACCCGTCTCTCAGAA CAAACTTTATCCGGTGATCTTACCGTTACCGCTTTAGCCCGT GGGTCCCTCCCACCGTGACTGCTTCCACCG	5334
	CGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGC GGGTAAACGGTAAGATCACCGGATAAAAGTTGTTCTGAGAAGACG GGTTGCCATAAAATTCAAAGATTGTTTGA	5335
	TTATCCGGTGATCTTAC	5336
	GTAAGATCACCGGATAA	5337
	AAAATCTTGAATTATGGCAACCCGTCTCTCGAACAAACTTA TCCGGCGATCTTAGCGTTACCGCTTTAGCCCGGTGGTCCTC	5338
20 Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Tyr15Term TAC-TAG	CCACCGTGACTGCTTCCACCGCCGTGTC GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGG CTAAAAGCGGGTAAACGCTAAGATGCCGGATAAAAGTTGTTCGG AGAAGACGGGTTGCCATAAAATTCAAAGATT	5339
	CGATCTTAGCGTTACC	5340
	GGTAAACGCTAAGATCG	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Leu17Term TTA-TAA	CTTGAATTATGGCAACCCGCTTCTCCGAACAAACTTATCCG GGCATCTTACCGTT <u>A</u> CCCGCTTTAGCCCGTGGGTCCCTCCCAC CGTACTGCTTCCACCGCCGTCGTCCCGA	5341
		TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCA CCGGGCTAAAAGCGGGT <u>A</u> ACGGTAAGATCGCCGGATAAAGTTG TTCGGAGAAAGACGGTTGCCATAAAATTCAAAG	5342
		TTACCGTT <u>A</u> CCCGCTT	5343
		AAGCGGGT <u>A</u> ACGGTAA	5344
10	Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Gly42Term GGA-TGA	CCGGTGGGTCTCCACCGTGA <u>C</u> GTACTGCTCCACCGCCGTCGTCCC GGAGATTCTCTCCTT <u>T</u> GACAACAAGCACC <u>G</u> GAACCAC <u>C</u> TCTCA CAACCCAAACCCACCGAGCA <u>T</u> TCACGATG	5345
		CATCGTGA <u>G</u> ATTGCTCGGTGGGTTGGGTGGTGAAGAGGTGGT TCCGGTGC <u>T</u> GTG <u>T</u> GT <u>C</u> <u>A</u> AAAGGAGAGAATCTCGGGACGACGGC GGTGGAA <u>G</u> AGCAGTCACGGTGGGAGGACCCACCGG	5346
		TCTCCTT <u>T</u> GACAACAA	5347
		TTGTTGT <u>C</u> <u>A</u> AAAGGAGA	5348
15	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Arg4Term CGA-TGA	ACATGAAGCAGTGAA <u>A</u> CTCTGTT <u>T</u> ATTGA <u>A</u> CTTATTAGTCTCA AACTATGA <u>A</u> TT <u>T</u> <u>C</u> <u>T</u> GACAAGAGAA <u>G</u> AGTTGA <u>A</u> GGTCAGTGTCCAG ATTTGTCTCATTGA <u>A</u> TTCTAAGTCGTGA	5349
		TCACGACTTAGA <u>A</u> TTCA <u>A</u> TGAGACAA <u>A</u> CTGGAA <u>C</u> ACTGAC <u>C</u> TTAC AAAC <u>T</u> CTCT <u>T</u> GT <u>C</u> <u>A</u> GA <u>A</u> ATT <u>C</u> ATAGTTGAGACTAATAAGATTCAA TACAAACAGAG <u>A</u> TTCA <u>T</u> CTGCTCATGT	5350
		TGA <u>A</u> TT <u>T</u> <u>C</u> <u>T</u> GACAAGAG	5351
		CTCTGT <u>C</u> <u>A</u> GA <u>A</u> ATTCA	5352
20	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Gln5Term CAA-TAA	TGAAGCAGTGAA <u>A</u> CTCTGTT <u>T</u> ATTGA <u>A</u> CTTATTAGTCTCAAAC TATGA <u>A</u> TT <u>CC</u> G <u>A</u> TA <u>A</u> GAGAGAA <u>G</u> AGTTGA <u>A</u> GGTCAGTGTCCAGATT TGTCTCATTGA <u>A</u> TTCTAAGTCGTGAAGC	5353
		GCTTCACGACTTAGA <u>A</u> TTCA <u>A</u> TGAGACAA <u>A</u> CTGGAA <u>C</u> ACTGAC <u>C</u> TACAA <u>A</u> CTCT <u>T</u> CT <u>T</u> <u>A</u> TCGGAA <u>A</u> TT <u>C</u> ATAGTTGAGACTAATAAGATT CA <u>A</u> TA <u>C</u> AA <u>A</u> CAGAG <u>A</u> TTCA <u>T</u> CTGCTCA	5354
		ATTTCCG <u>A</u> TA <u>A</u> GAGAGA <u>A</u> G	5355
		CTTCTCT <u>T</u> ATCGGAA <u>A</u> T	5356
25	Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG	AGCAGTGAA <u>A</u> CTCTGTT <u>T</u> ATTGA <u>A</u> CTTATTAGTCTCAAAC <u>T</u> GA <u>A</u> TT <u>CC</u> G <u>A</u> CA <u>A</u> <u>A</u> AG <u>A</u> AGTTGA <u>A</u> GGTCAGTGTCCAGATT <u>T</u> CTCATTGA <u>A</u> TTCTAAGTCGTGAAG <u>C</u> TTA	5357
		TAAGCTTCACGACTTAGA <u>A</u> TTCA <u>A</u> TGAGACAA <u>A</u> CTGGAA <u>C</u> ACTGA CCTTACAA <u>A</u> CT <u>T</u> CT <u>A</u> TTGT <u>CGG</u> <u>A</u> ATT <u>C</u> ATAGTTGAGACTAATAA GATT <u>C</u> A <u>A</u> ACAGAG <u>A</u> TTCA <u>T</u> CTGCT	5358
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACAATAGAAGTTT	5359
	AAACTTCTATTGTCGGA	5360
5 Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Lys7Term AAG-TAG	AGTGAAATCTCTGTTGTATTGAATCTTATTAGTCTCAAACATATGAA TTTCCGACAAGAGTAGTTGTAAGGTCAGTGTCCAGATTGTCTC ATTGAATTCTAAGTCGTGAAGCTTAATT AATTAAGCTTCACGACTAGAATTCAATGAGACAAATCTGGAACAC TGACCTTACAAACTACTCTTGTGGAAATTCAAGTTGAGACTAA TAAGATTCAATACAAACAGAGATTCACT GACAAGAGTAGTTGTA	5361 5362 5363 5364
10 Lead Tolerance cyclic nucleotide-regulated ion channel <i>Arabidopsis thaliana</i> Gln12Term CAA-TAA	CATTGAATTCTAAGTCGTGAAGCTTAATTGATTCTCTTCACTTTC TCGGATCAGGTTTAAGATTGGAAGTCGGATAAGACTTCCCTCGA CGTGGAAATTCCCGTAAAAACGAGATT GAATCTCGTTTACCGGAATATTCCACGTCGGAGGAAGTCTTATC CGACTTCCAATCTTAAACCTGATCCGAGAAAGTGAAGAAGAATC GAATTAAGCTTCACGACTAGAATTCAATG TCAGGTTTAAGATTGG	5365 5366 5367 5368
15 Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln5Term CAA-TAA	TGGAAGTCAATCCCCACGTTGAGCAGGTTGATGCATTGGCTAA GTTATGAATCACCGCTAAGACGAGTTGAGGTTTCAGGATTGG AAATCAGAGAGAAGCTCTGAGGGAAATTTC GAAAATTCCCTCAGAGCTCTCTCTGATTCCAATCCTGAAACCT CACAAACTCGTCTTACCGGTGATTCTAACTTTAGCCAATGCATCA ACCTGCTCAACGTGGGGATTGACTTCCA ATCACCGCTAAGACGAG	5369 5370 5371 5372
20 Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gly7Term GAG-TAG	TCATCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATG AATCACCGCCAAGACTAGTTGAGGTTTCAGGATTGGAAATCA GAGAGAAGCTCTGAGGGAAATTTCATGCTA TAGCATGAAAATTCCCTCAGAGCTCTCTGATTCCAATCCTG AAACCTCACAAACTAGTCTGGCGGTGATTCTAACTTTAGCCAAT GCATCACCTGCTAACGTGGGGATTGA GCCAAGACTAGTTGTG	5373 5374 5375 5376

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln12Term CAG-TAG	GAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGAC GAGTTTGTGAGGTTT <del>T</del> AGGATTGGAAATCAGAGAGAAGCTCTGAG GGAAATTTCATGCTAAAGGTGGAGTCCACC	5377
	GGTGGACTCCACCTT <del>T</del> AGCATGAAAATTCCCTCAGAGCTCTCTC TGATTTC <del>A</del> ATCCTAAAACCTCACAAACTCGTCTGGCGGTGATT	5378
	TGAGGTTT <del>T</del> AGGATTGG	5379
	CCAATCCT <del>A</del> AAACCTCA	5380
10 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Trp14Term TGG-TGA	TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTGT GAGGTT <del>T</del> CAGGATTG <del>T</del> AAATCAGAGAGAAGCTCTGAGGGAAATT TCATGCTAAAGGTGGAGTCCACC <del>G</del> GAAGTAA	5381
	TTTACTTCGGTGGACTCCACCTT <del>T</del> AGCATGAAAATTCCCTCAGAG CTTCTCTGATT <del>A</del> CAATCCTGAAACCTCACAAACTCGTCTGGC GGTGATT <del>C</del> ATAACTT <del>T</del> AGCCAATGCATCA	5382
	CAGGATTG <del>T</del> AAATCAGA	5383
	TCTGATT <del>T</del> ACAATCCTG	5384
15 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Lys15Term AAA-TAA	GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTGT AGGTT <del>T</del> CAGGATTG <del>G</del> TAATCAGAGAGAAGCTCTGAGGGAAATT CATGCTAAAGGTGGAGTCCACC <del>G</del> GAAGTAAAG	5385
	CTTTACTTCGGTGGACTCCACCTT <del>T</del> AGCATGAAAATTCCCTCAGA GCTTCTCTGATT <del>A</del> CAATCCTGAAACCTCACAAACTCGTCTGG CGGTGATT <del>C</del> ATAACTT <del>T</del> AGCCAATGCATC	5386
	AGGATTG <del>G</del> TAATCAGAG	5387
	CTCTGATT <del>A</del> CAATCCT	5388
20 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu2Term GAA-TAA	CTTGAAGAATTGATCTACCACTCTAGCTGCTAACTGTTGCC <del>T</del> GG TGGAGATAATGATG <del>T</del> AAAGAGAGGACAGATATGTTAGATT <del>C</del> AGGA CTGCAAATCAGAGCAATCTGTTATCTCAG	5389
	CTGAGATAACAGATTGCTCTGATT <del>T</del> GCAGTCCTGAAATCTAACATA TCTGTCCTCTTT <del>A</del> CATCATTATCTCCACCAGGCGAACAGTAGC AGCTAAGAGTGGTAGATCAATTCTCAAG	5390
	TAATGATG <del>T</del> AAAGAGAG	5391
	CTCTCTT <del>A</del> CATCATT	5392

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg3Term AGA-TGA	GAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTGCCCTGGTG GAGATAATGATGGA <u>TGAGAGGACAGATATGTTAGATTCAGGAC</u> TGCAAATCAGAGCAATCTTATCTCAGAGA	5393
		TCTCTGAGATAACAGATTGCTCTGATTGCAGTCCTGAAATCTAAC ATATCTGTCCTCTCA <u>ATCCATCATTATCTCCACCAGGCGAACAGTT</u> AGCAGCTAAGAGTGGTAGATCAATTCTTC	5394
		TGATGGA <u>ATGAGAGGAC</u>	5395
		GTCCTCTC <u>ATTCATCA</u>	5396
10	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu4Term GAG-TAG	GAATTGATCTACCACTCTTAGCTGCTAACTGTTGCCCTGGTGGAG ATAATGATGGA <u>AGATAGGACAGATATGTTAGATTCAGGACTGCA</u> AATCAGAGCAATCTTATCTCAGAGAACG	5397
		CGTTCTCTGAGATAACAGATTGCTCTGATTGCAGTCCTGAAATCT AACATATCTGTCCT <u>ATCTTCCATCATTATCTCCACCAGGCGAACAA</u> GTTAGCAGCTAAGAGTGGTAGATCAATT	5398
		TGGAAAG <u>ATAGGACAGA</u>	5399
		TCTGTCCT <u>ATCTTCCA</u>	5400
15	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg6Term AGA-TGA	ATCTACCACTCTTAGCTGCTAACTGTTGCCCTGGTGGAGATAATG ATGGAAAGAGAGG <u>ACTGATATGTTAGATTCAGGACTGCAAATCA</u> GAGCAATCTTATCTCAGAGAACGCA <u>AGTT</u>	5401
		AAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTGCAGTCCTG AAATCTAACATATC <u>AGTCCTCTTCCATCATTATCTCCACCAGG</u> CGAACAGTTAGCAGCTAAGAGTGGTAGAT	5402
		GAGAGG <u>ACTGATATGTT</u>	5403
		AACATATC <u>AGTCCTCTC</u>	5404
20	Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Tyr7Term TAT-TAG	CCACTCTTAGCTGCTAACTGTTGCCCTGGTGGAGATAATGATGGA AAGAGAGGACAGAT <u>AGGTTAGATTCAGGACTGCAAATCAGAGCA</u> ATCTTATCTCAGAGAACGCA <u>AGTT</u> TGTTGAAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTGCAG	5405
		TCCTGAAATCTAAC <u>CTATCTGTCCTCTTCCATCATTATCTCCAC</u> CAGGCGAACAGTTAGCAGCTAAGAGTGG	5406
		GACAGATA <u>GGTTAGATT</u>	5407
		AATCTAAC <u>CTATCTGTC</u>	5408
25	2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu2Term GAG-TAG	ATCCTTCTCTGAGAAAAAACACAGATCCGA <u>ATTTATCTTAA</u> GCCGGAAAAATG <u>TAGAAAGCGATCGAGAGACAACCGCGTTCTT</u> TGAGCATCTCCGAC <u>CTTCTTCTTCTT</u>	5409
		AAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACCGCGTTGTC TCTCGATCG <u>CTTCTACATTTTCCGGCTGATTAAGATAAAATTC</u> GGATCTGTTGTTTCTCAGAGAAGGAT	5410

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	AAAAAATGTAGAAAGCG	5411
	CGCTTTCTACATTTTT	5412
5 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Lys3Term AAA-TAA	CTTCTCTGAGAAAAACACAGATCCGAATTTATCTTTAATCAGC CGGAAAAAAATGGAGTAAGCGATCGAGAGACAACGCGTCTCTTG AGCATCTCCGACCTCTTCTTCTTCTCGC	5413
	GCGAAGAAGAAGAAGAAGGTGGAGATGCTCAAGAAGAACCGT TGTCTCTCGATCGCTTACTCCATTTCGGCTGATTAAGATAA AATCGGATCTGTTGTTCTCAGAGAAG	5414
	AAATGGAGTAAGCGATC	5415
	GATCGCTTACTCCATT	5416
	GAAAAAACACAGATCCGAATTTATCTTTAATCAGCCGGAAAAAA TGGAGAAAGCGATCTAGAGACAAACGCGTCTTCTTGAGCATCTCC GACCTTCTCTTCTTCTCGCACAATTACG	5417
10 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG	CGTAATTGTGCGAAGAAGAAGAAGAGTGGAGATGCTCAAGAA GAACGCGTTGTCTCTAGATCGCTTCTCCATTTCGGCTGATT AAAGATAAAATCGGATCTGTTGTTTC	5418
	AAGCGATCTAGAGACAA	5419
	TTGTCTCTAGATCGCTT	5420
	AAAACAACAGATCCGAATTTATCTTTAATCAGCCGGAAAAATGG AGAAAGCGATCGAGTGACAACGCGTCTTCTTGAGCATCTCCGAC CTTCTCTCTTCTCGCACAATTACGAGG	5421
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Arg7Term AGA-TGA	CCTCGTAATTGTGCGAAGAAGAAGAAGAGTGGAGATGCTCAA GAAGAACCGCGTTGTCACTCGATCGCTTCTCCATTTCGGCT GATTAAGATAAAATCGGATCTGTTGTTT	5422
	CGATCGAGTGACAACGC	5423
	GCGTTGTCACTCGATCG	5424
	ACAACAGATCCGAATTTATCTTTAATCAGCCGGAAAAATGGAGA AAGCGATCGAGAGATAACGCGTCTTCTTGAGCATCTCCGACCTT CTTCTCTCTCGCACAATTACGAGGCTT	5425
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA	AAGCCTCGTAATTGTGCGAAGAAGAAGAAGAGTGGAGATGCT CAAGAAGAACCGCGTTATCTCTCGATCGCTTCTCCATTTCGG CTGATTAAGATAAAATCGGATCTGTTGT	5426
	TCGAGAGATAACGCGTT	5427
	AACGCGTTATCTCTCGA	5428

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Glu26Term GAA-TAA	GAGAGACAAAGAGTTCTTCTGAACATCTCGCCTTCTTCTT CCTCTCACAGCTTTAAGGCTCTCTCTGCTTCAGCTTGCTGGC TGGGGACAGTGCTGCGTATCAGAGGACCT	5429
	AGGTCTCTGATACCGCAGCACTGTCCCCAGCCAAGCAAGCTGAA GCAGAGAGAGAGCCTTAAAAGCTGTGAGAGGAAGAAGAAGAAGG ACGGAGATGTTCAAGAAGAACTCTTGTCTCTC	5430
	ACAGCTTTAAGGCTCT	5431
	AGAGCCTTAAAAGCTGT	5432
10 2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Ser32Term TCA-TGA	TTGAACATCTCCGCTCTTCTTCTCACAGCTTGAGG CTCTCTCTGCTTGGCTGGGACAGTGCTGCGTA TCAGAGGACCTCTCTATGGAGATGATGT	5433
	ACATCATCTCCATAGAGAGAGGCTCTGATACGCAGCACTGTCC CCAGCCAAGCAAGCTCAAGCAGAGAGAGCCTTCAAAGCTGTG AGAGGAAGAAGAAGAAGGACGGAGATGTTCAA	5434
	CTCTGCTTGGCTTGCT	5435
	AGCAAGCTCAAGCAGAG	5436
	TCTCCGCTCTTCTTCTCACAGCTTGAGGCTCTC TCTGCTCAGCTTGTGGCTGGGACAGTGCTGCGTATCAGAG GACCTCTCTATGGAGATGATGTAGTCATT	5437
15 20 2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Cys34Term TGC-TGA	AATGACTACATCATCTCCATAGAGAGAGGCTCTGATACGCAGC ACTGTCCCCAGCCAATCAAGCTGAAGCAGAGAGAGCCTTCAA GCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5438
	TCAGCTTGATTGGCTGG	5439
	CCAGCCAATCAAGCTGA	5440
	TCCGTCTTCTTCTTCTCACAGCTTGAGGCTCTC TGCTCAGCTTGTAGGCTGGGACAGTGCTGCGTATCAGAGGA CCTCTCTATGGAGATGATGTAGTCATTGT	5441
25 2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Leu35Term TTG-TAG	ACAATGACTACATCATCTCCATAGAGAGAGGCTCTGATACGCA GCACTGTCCCCAGCCTAGCAAGCTGAAGCAGAGAGAGCCTC AAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5442
	AGCTTGCTAGGCTGGGG	5443
	CCCCAGCCTAGCAAGCT	5444

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Tyr42Term TAT-TAG	TCACAGCTTGAAGGCTCTCTCTGCTTCAGCTTGCTGGCTGG GGACAGTGCTGCGTAGCAGAGGACCTCTCTATGGAGATGATGT AGTCATTGTTGCGGCACATAGGACTGCACTA	5445
	TAGTCAGTCCTATGTGCCGCAACAATGACTACATCATCTCCATA GAGAGAGGTCTCTGCTACGCAGCACTGCCCCAGCCAAGCAAG CTGAAGCAGAGAGAGAGCCTCAAAGCTGTGA	5446
	GCTGCGTAGCAGAGGAC	5447
	GTCCTCTGCTACGCAGC	5448
10 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr25Term TAC-TAG	CAACAGACAGCAAGTGTGCTCCAGCATCTCGCCCTTCTAATT TTCTTCTCACAAATTAGGAGTCCGCTTGCAGCATCAGTATGTGCT GCAGGGGATAGCGCCGCATATCATAGGGCT	5449
	AGCCCTATGATATGCGCGCTATCCCCTGCAGCACATACTGATGC GGCAAGAGCGGACTCTAATTGTGAGAAGAAGAATTAGAAGGGC GGAGATGCTGGAGAACACTTGCTGTCTGTT	5450
	CACAATTAGGAGTCCGC	5451
	GCGGACTCTAATTGTG	5452
	AACAGACAGCAAGTGTGCTCCAGCATCTCGCCCTTCTAATT CTTCTCACAAATTACTAGTCCGCTTGCAGCATCAGTATGTGCT CAGGGGATAGCGCCGCATATCATAGGGCT	5453
15 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Glu26Term GAG-TAG	AAGCCCTATGATATGCGCGCTATCCCCTGCAGCACATACTGATG CGGCAAGAGCGGACTAGTAATTGTGAGAAGAAGAATTAGAAGGG CGGAGATGCTGGAGAACACTTGCTGTCTGTT	5454
	ACAATTACTAGTCCGCT	5455
	AGCGGACTAGTAATTGT	5456
	TCCAGGCATCTCCGCCCTCTAATTCTTCTCACAATTACGAGTC CGCTCTTGCAGCATGAGTATGTGCTGCAGGGGATAGCGCCGCAT ATCATAGGGCTCTGTTATGGAGACGATGT	5457
20 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Ser32Term TCA-TGA	ACATCGTCTCCATAAACAGAAGCCCTATGATATGCGCGCTATCC CCTGCAGCACATACTCATGCAGCAAGAGCGGACTCGTAATTGTGA GAAGAAGAATTAGAAGGGCGGAGATGCTGGA	5458
	TGCCGCATGAGTATGTG	5459
	CACATACTCATGCAGCA	5460

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Cys34Term TGT-TGA	TCTCCGCCCTCTAATTCTCTTCACAATTACGAGTCCGCTCTT GCCGCATCAGTATGAGCTGCAGGGATAGCGCCGCATATCATAG GGCTTCTGTTATGGAGACGATGTGGTGATT	5461
	AATCACACATCGTCCATAAACAGAACGCCATGATATGCCGC GCTATCCCCTGCAGCICATACTGATGCCCAAGAGCGGACTCGT AATTGTGAGAAGAAGAATTAGAAGGGCGGAGA	5462
	TCAGTATGAGCTGCAGG	5463
	CCTGCAGCICATACTGA	5464
10 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr42Term TAT-TAG	TCACAATTACGAGTCCGCTTGCAGCATCAGTATGCTGCAGG GGATAGCGCCGCATAGCATAGGGCTTCTGTTATGGAGACGATGT GGTGATTGGCAGCTCATCGTACTGCACCT	5465
	AAGTCAGTACGATGAGCTGCCAACATACCACATCGTCCATA AACAGAACCCATGCTATGCCGCATCCCCTGCAGCACATAC TGATGCCAGAAGAGCGGACTCGTAATTGTGA	5466
	GCCGCATAGCATAGGGC	5467
	GCCCTATGCTATGCCGC	5468
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Tyr22Term TAC-TAG	GAAGGCAGTCAACAGGCAGAGCATTGCTACATCATCTCCGGCC TTCTTCTCCGCTTAGACAAATGAATCTCGCTCTGCATCGTT TGTGCAGCTGGGATAGTGCCTCGTATCAA	5469
	TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCTTGTCTAAGCGGAAGAAGAAGGCCGGAGATGATG TAGCAAAATGCTCTGCCCTGTTGATGCCCTTC	5470
	TCCGCTTAGACAAATGA	5471
	TCATTTGTCTAAGCGGA	5472
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTGCTACATCATCTCCGGCCTCTT CCGCTTACACAAATTATCTCGCTCTGCATCGTTGTGCAGC TGGGGATAGTGCCTCGTATCAAAGGACAT	5473
	ATGTCCTTGATACGAAGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATTGTGTAAGCGGAAGAAGAAGGCCGG AGATGATGAGCAAATGCTCTGCCCTGTTGAT	5474
	ACACAAATTAAATCTCG	5475
	CGAAGATTAAATTGTGT	5476

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser27Term TCG-TAG	GGCAGAGCATTTGCTACATCATCTCCGGCCTTCTCCGCTTA CACAAATGAATCTT <u>AGCTCTCGCATCGGTTGTGCAGCTGGGGA</u> TAGTGCTTCGTATCAAAGGACATCGGTGTT	5477
	AACACCGATGTCCTTGATACGAAGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCT <u>TAAGATTCA</u> TTGTGTAAGCGGAAGAAGAA GGCCGGAGATGATGTAGCAAAATGCTCTGCC	5478
	TGAATCTT <u>AGCTCTCTG</u>	5479
	CAGAGAGCT <u>TAAGATTCA</u>	5480
10 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCTCCGCTTACACAAATGAATC TTCGCTCTGCAT <u>AGGTTTGTGCAGCTGGGATAGTGCTTCGTA</u> TCAAAGGACATCGGTGTTGGAGATGATGT	5481
	ACATCATCTCCAAACACCGATGTCCTTGATACGAAGCACTATCCC CAGCTGCACAAACCT <u>ATGCAGAGAGCGAAGATTCA</u> TTGTGTAAG CGGAAGAAGAAGGCCGGAGATGATGTAGCA	5482
	CTCTGCAT <u>AGGTTTGTG</u>	5483
	CACAAACCT <u>ATGCAGAG</u>	5484
	TCATCTCCGGCCTTCTCCGCTTACACAAATGAATCTCGCTC TCTGCATCGGTT <u>GAGCAGCTGGGATAGTGCTTCGTATCAAAGG</u> ACATCGGTGTTGGAGATGATGTGATT	5485
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Cys33Term TGT-TGA	AATCACGACATCATCTCCAAACACCGATGTCCTTGATACGAAGCA CTATCCCCAGCTGC <u>CAAACCGATGCAGAGAGCGAAGATTCA</u> TT GTGTAAGCGGAAGAAGAAGGCCGGAGATGA	5486
	TCGGTTT <u>GAGCAGCTGG</u>	5487
	CCAGCTGC <u>CAAACCGA</u>	5488
	GAAGGCAATCAACAGGGCAGAGCATTCTGCTACATCATCTCCGGCC TTCATCTCGGCTT <u>AGGCCATGAATCTCGCTCTGCATCGGTT</u> TGTGCAGCTGGGATAGTGCGCGTATCAA	5489
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Tyr22Term TAT-TAG	TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATT <u>CATGGCTCAAGCCGAAGATGAAGGCCGGAGATGAT</u> GTAGCAGAATGCTCTGCCTGTTGATTGCCTTC	5490
	TCGGCTT <u>AGGCCATGA</u>	5491
	TCATGGCT <u>CAAGCCGA</u>	5492

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTT CGGCTTATGCCATTAAATCTCGCTCTGCATCGGTTGTGCAG CTGGGGATAGTGCCTCGTATCAAAGAACGT	5493
	ACGTTCTTGATACGACGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATGGCTATAAGCCGAAGATGAAGGCCGG AGATGATGAGCAGAATGCTCTGCCTGTTGAT	5494
	ATAGCCATTAAATCTTCG	5495
	CGAAGATTAAATGGCTAT	5496
10 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Ser27Term TCG-TAG	GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTCGGCTT ATAGCCATGAATCTTAGCTCTGCATCGGTTGTGCAGCTGGGG ATAGTGCCTCGTATCAAAGAACGTCGGTGT	5497
	AACACCGACGTTCTTGATACGACGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCAAGCCGAAGATGAA GGCCGGAGATGATGAGCAGAATGCTCTGCC	5498
	TGAATCTTAGCTCTCG	5499
	CAGAGAGCTAAGATTCA	5500
	TGCTACATCATCTCCGGCCTTCATCTTGGCTTATAGCCATGAATC TTCGCTCTGCATAGGTTGTGCAGCTGGGGATAGTGCCTCGTA TCAAAGAACGTCGGTGTGGAGATGATGT	5501
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Ser31Term TCG-TAG	ACATCATCTCAAACACCGACGTTCTTGATACGACGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCAAG CCGAAGATGAAGGCCGGAGATGATGTAGCA	5502
	CTCTGCATAGGTTGTG	5503
	CACAAACCTATGCAGAG	5504
	TCATCTCCGGCCTTCATCTTGGCTTATAGCCATGAATCTCGCTC TCTGCATCGGTTGAGCAGCTGGGGATAGTGCCTCGTATCAAAGA ACGTCGGTGTGGAGATGATGTCGTGATA	5505
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Cys33Term TGT-TGA	TATCACGACATCATCTCAAACACCGACGTTCTTGATACGACGCA CTATCCCCAGCTGCCTAAACCGATGCAGAGAGCGAAGATTCAAG CTATAAGCCGAAGATGAAGGCCGGAGATGA	5506
	TCGGTTGAGCAGCTGG	5507
	CCAGCTGCTCAAACCGA	5508
	TCATAGTCCTTGGCGCTGGATTCTCCAAGGTAGTGAGCTG CTATGGCAACTCATAGCAAACGCAACCTCCTCCGATTTCCCG CTCTGCCGATGAAAATCCAGATTCCAG	5509
25 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i>	CTGGAATCTGGGAATTTCATCGGCAAGAGCGGGAAAATCGGAAG	5510
	GAGGTTGCCTTGCTAATGAGTTGCCATAGCAGCTCACTAACCTT GGAAGAATCCAAGCGGCAAAAGAGACTATGA	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CAACTCAT <u>TAGCAAACG</u>	5511
	CGTTTGCT <u>AATGAGTTG</u>	5512
5 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln6Term CAA-TAA	TAGTCTCTTTGCCGCTGGATTCTCCAAGGTTAGTGAGCTGCTA TGGCAACTCATCAG <u>TAACGCAACCTCCTCCGATTTCCCGCTC</u> TTGCCGAT <u>AAAAATTCCAGATTCAGGTT</u> AACCTGGAATCTGGGAATTTCATCGGCAAGAGCAGGGAAAATCGG AAGGAGGTTGC <u>GT</u> <u>TTACTGATGAGTTGCCATAGCAGCTCACTAAC</u> CTTGGAAAGAATCCAAGCGGCAAAGAGACTA CTCATCAG <u>TAACGCAA</u>	5513 5514 5515 5516
10 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA	CTTTGCCGCTGGATTCTCCAAGGTTAGTGAGCTGCTATGCC ACTCATCAGCAA <u>ACGTAACCTCCTCCGATTTCCCGCTTGC</u> GAT <u>AAAAATTCCAGATTCAGGTTCAATT</u> AAATTGAACCTGGAATCTGGGAATTTCATCGGCAAGAGCAGGGAA AATCGGAAGGAGGTT <u>ACGTTGCTGATGAGTTGCCATAGCAGCTC</u> ACTAACCTGGAAAGAATCCAAGCGGCAAAG AGCAA <u>ACGTAACCTCCT</u> AGGAGGTT <u>ACGTTGCT</u>	5517 5518 5519 5520
15 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Glu19Term GAA-TAA	GCTGCTATGGCAACTCATCAGCAA <u>ACGCAACCTCCTCCGATTT</u> CCCGCTCTGCCGAT <u>AAAATTCCAGATTCAGGTTCAATTACA</u> CCTTCTAATCATTATTCTTAATT <u>TTCT</u> AAGAAAAATTAAAGAAATAATGATTAGAAGGTGTAATT <u>GAACCTGG</u> AATCTGGGAATT <u>TAATCGGCAAGAGCAGGGAAAATCGGAAGGAG</u> GTTGCGTTGCTGATGAGTTGCCATAGCAGC TTGCCGAT <u>AAAATTCC</u> GGAATT <u>TTAATCGGCAA</u>	5521 5522 5523 5524
20 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln22Term CAG-TAG	GCAACTCATCAGCAA <u>ACGCAACCTCCTCCGATTTCCCGCTT</u> GCCGAT <u>AAAATTCC</u> <u>TAGATTCCAGGTTCAATTACACCTTCTAAT</u> CATTATTCTTAATT <u>TTCTTGTTGGATT</u> AATCCACCAA <u>AGAAAAATTAAAGAAATAATGATTAGAAGGTGTAATT</u> GAACCTGGAA <u>ATCTAGGAATTTCATCGGCAAGAGCAGGGAAAATCG</u> GAAGGAGGTTGC <u>GT</u> <u>TTGCTGATGAGTTGC</u> AAAATT <u>CCTAGATTCCA</u> TGGAAT <u>CTAGGAATT</u>	5525 5526 5527 5528

**Example 8****Production of albino mutants for the analysis of photosynthetic processes**

Plant productivity is limited by resources available and the ability of plants to harness these resources. The conversion of light to chemical energy, which is then used to synthesize carbohydrates, fatty acids, sugars, amino acids and other compounds, requires a complex system which combines the light harvesting apparatus of pigments and proteins. The value of light energy to the plant can only be realized when it is efficiently converted into chemical energy by photosynthesis and fed into various biochemical processes. Significant effort has therefore been directed at studying photosynthetic processes in plants in order to improve productivity and/or the efficiency of photosynthesis. The analysis of the photosynthetic process is substantially aided by the ability to produce albino plants.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

**Table 18**  
**Oligonucleotides to produce albino plants**

	<b>Phenotype, Gene, Plant &amp; Targeted Alteration</b>	<b>Altering Oligos</b>	<b>SEQ ID NO:</b>
5	White leaves Immutans <i>Arabidopsis thaliana</i> Ser5Term TCA-TGA	TTCTTCTGTGAAATTATCTGCTCAAATCTTGGTCTGACGGAG ATGGCGCGATTTGAGGCATCTCCTCTGGTACGTTGACGATTCA CGGCCTTGGTACTCTCGACGCTCTAG	5529
		CTAGAGCGTCAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTA CCAGAGGAGATGCCTCAAATGCCGCCATCTCCGTAGGAACCAA	5530
		AGATTGAGCAGATAATTACAGGAAAGAA	
		GGCGATTGAGGCATCT	5531
		AGATGCCTCAAATGCC	5532
10	White leaves Immutans <i>Arabidopsis thaliana</i> Leu12Term TTG-TAG	GCTCAAATCTTGGTCTGACGGAGATGGCGCGATTCTAGGCA TCTCCTCTGGTACGTAGACGATTTCACGGCCTTGGTACTCTCG ACGCTCTAGAGCCGCCGTTCTGACAGCTC	5533
		GAGCTGTACGAAACGGCGGCTCTAGAGCGTCAAGAGTAACCAA GGCCGTGAAATCGTCTACGTACCGAGAGGAGATGCCTGAAATGCC	5534
		GCCATCTCCGTCAAGAACCAAAGATTGAGC	
		TGGTACGTAGACGATT	5535
		AAATCGTCTACGTACCA	5536
15	White leaves Immutans <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA	TTGGTCTGTACGGAGATGGCGCGATTCTAGGCATCTCCTCTG GTACGTTGACGATTGACGGCCTTGGTACTCTCGACGCTCTAG AGCCGCCGTTCTGACAGCTCTCACC	5537
		CGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTCAAG AGTAACCAAAGGCCGTCAAATCGTCAACGTACCGAGAGGAGATGCC	5538
		TGAAATGCCGCCATCTCCGTCAAGAACCAAAG	
		GACGATTGACGGCCTT	5539
		AAGGCCGTCAAATCGTC	5540
20	White leaves Immutans <i>Arabidopsis thaliana</i> Arg22Term CGA-TGA	GCGCGATTCAGGCATCTCCTCTGGTACGTTGACGATTACCG CCTTGGTACTCTTGACGCTCTAGAGCCGCCGTTCTGACAGCT CCTCTACCGATTGCTTCATCATCTCCTC	5541
		GAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACG GCGGCTCTAGAGCGTCAAAGAGTAACCAAAGGCCGTGAAATCGTC	5542
		AACGTACCAAGAGGAGATGCCTGAAATGCCGC	
		TTACTCTTGACGCTCT	5543
		AGAGCGTCAAAGAGTAA	5544
25			

5	White leaves Immutans <i>Arabidopsis thaliana</i> Arg25Term AGA-TGA	TCAGGCATCTCCTCTGGTACGTTGACGATTCACGGCCTTGGTTA CTCTTCGACGCTCTTGAGCCGCCGTTCGTACAGCTCTCTCACC GATTGCTTCATCATCTCCTCTCTC	5545
		GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTG TACGAAACGGCGGCTCAAGAGCGTCGAAGAGTAACCAAAGGCCG TGAAATCGTCAACGTACCAGAGGAGATGCCTGA	5546
		GACGCTCTTGAGCCGCC	5547
		GGCGGCTCAAGAGCGTC	5548
		GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTCGATT CTGCTATGAGTTTGAACCTCAGTTCTCATATTCTGTTAGA GCTAGGAGTTTGAGAAGTCATCAGTT	5549
10	White leaves Immutans <i>Lycopersicon esculentum</i> Gly11Term GGA-TGA	AAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGAATATGAA GAAACTGAGGTTCAAAACTCATAGCAGAAATCGAAATGCCATT TTGATCCTCTTCCCTCCCACAAGAAC	5550
		TGAGTTTGAACCTCA	5551
		TGAGGTTCAAAACTCA	5552
		GTGGGAAGGAAGAAGGATCAAGAATGGCGATTCGATTCTGCTA TGAGTTTGGAACCTGAGTTCTCATATTCTGTTAGAGCTAGG AGTTTGAGAAGTCATCAGTTATGCAA	5553
		TTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGA ATATGAAGAAACTCAGGTTCCAAAACTCATAGCAGAAATCGAAATC GCCATTCTGATCCTCTTCCCTCCCAC	5554
15	White leaves Immutans <i>Lycopersicon esculentum</i> Ser13Term TCA-TGA	TGGAACCTGAGTTCTT	5555
		AAGAAACTCAGGTTCCA	5556
		AAGAAGGATCAAGAATGGCGATTCGATTCTGCTATGAGTTGG AACCTCAGTTCTGATATTCTGTTAGAGCTAGGAGTTGAGA AGTCATCAGTTATGCAATTCCCAGAA	5557
		TTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTC TAAAACAAGAATATCAAGAAACTGAGGTTCCAAAACTCATAGCAGA AATCGAAATGCCATTCTGATCCTCTT	5558
		AGTTCTGATATTCTT	5559
20	White leaves Immutans <i>Lycopersicon esculentum</i> Ser16Term TCA-TGA	AAGAATATCAAGAAACT	5560
		AGGATCAAGAATGGCGATTCGATTCTGCTATGAGTTGGAAC TCAGTTCTCATAGCTTGTTAGAGCTAGGAGTTGAGAAGTC ATCAGTTTATGCAATTCCCAGAACCA	5561
		TGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTA GCTCTAAAACAAGACTATGAAGAAACTGAGGTTCCAAAACTCATAG CAGAAATCGAAATGCCATTCTGATCCT	5562
		TCTTCATAGCTTGTT	5563
		AAACAAGACTATGAAGA	5564
25	White leaves Immutans <i>Lycopersicon esculentum</i> Tyr17Term TAT-TAG		

5	White leaves Immutans <i>Lycopersicon esculentum</i> Cys19Term TGT-TGA	AAGAATGGCGATTCGATTCGCTATGAGTTTGGAACCTCAGTTCTTCATATTCTGATTAGAGCTAGGAGTTGAGAAGTCATCAGTTTATGCAATTCCCAGAACCCATGTCGG	5565
		CCGACATGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAATCAAGAATATGAAGAAACTGAGGTTCCAAAAC	5566
		TCATAGCAGAAATCGAAATGCCATTCTT	
		TATTCTTGATTAGAGC	5567
		GCTCTAAATCAAGAATA	5568
10	White leaves Immutans <i>Capsicum annuum</i> Ser13Term TCA-TGA	CGCGTCCGATAAAAAAAATCAAGAATGGCGATTCATATCTGCTATGAGTTTCAACTTGCATATTCTTCATATTCAAGCATTGGCAATTCCAAAGAACCCATTCAAGAACCCATTGGTTGAATT	5569
		GAATTCAAACAAATGGGTTCTTGGATTGCACAAAAATGCTGAATATGAAGAAGAAACTCAAGTTGCAAAACTCATAGCAGATATGGAAATCGCCATTCTGATTGGACGCG	5570
		TCGAACATTGAGTTCTT	5571
		AAGAAACTCAAGTTGCA	5572
15	White leaves Immutans <i>Capsicum annuum</i> Ser17Term TCA-TGA	AAAAATCAAGAATGGCGATTCATATCTGCTATGAGTTTCAACTTCAGTTCTCTATTTCACT	5573
		TCAGTTCTTCTGATATTCAAGCATTGGCAATTCCAAAGAACCCATTGGTTGAATTCTCTATTTCACT	
		AGTAAAATAGAGAATTCAAACAAATGGGTTCTTGGATTGCACA	5574
		AAAATGCTGAATATCAAGAAGAAACTGAAGTTGCAAAACTCATAGCAGATATGGAAATGCCATTCTGATT	
		TTCTTCTTGAATTCAAG	5575
20	White leaves Immutans <i>Capsicum annuum</i> Ser19Term TCA-TGA	CTGAATATCAAGAAGAA	5576
		CAAGAATGGCGATTCATATCTGCTATGAGTTTCAACTTCAGTTCTTCATATTGAGCATTGGCAATTCCAAAGAACCCATTGGTTGAATTCTCTATTTCACTTAGGAA	5577
		TTCTTCTTCTGCAATTCCAAAGAACCCATTGGTTGAATTCTCTATTTCACTTAGGAA	
		TTCTTAAGTGAAAATAGAGAATTCAAACAAATGGGTTCTTGGATTGCACAAAAATGCTCAATATGAAGAAGAAACTGAAGTTGCAAAACTCATAGCAGATATGGAAATGCCATTCTG	5578
		TTCATATTGAGCATT	5579
25	White leaves Immutans <i>Capsicum annuum</i> Leu21Term TTG-TAG	AAAATGCTCAATATGAA	5580
		CGATTCATATCTGCTATGAGTTTCAACTTCAGTTCTTCATATTCAAGAACCCATTGGTTGAATTCTCTATTTCACTTAGGAAATTCTCATAG	5581
		CTATGAGAATTCTAAGTGAAAATAGAGAATTCAAACAAATGGGTTCTTGGATTGCACAAAAATGCTGAATATGAAGAAGAAACTGAAGTTCGAAACTCATAGCAGATATGGAAATCG	5582
		AGCATTGGTGAATT	5583
		AATTGCACTAAAATGCT	5584

5	White leaves Immutans <i>Capsicum annuum</i> Cys22Term TGC-TGA	TTCCATATCTGCTATGAGTTTCGAACCTCAGTTCTTCTTCATATT CAGCA <del>TTTGTGAA</del> ATTCCAAGAACCCAT <del>TTTGTGAA</del> TTCTCA TTTCACCTAGGAATTCTCATAGAACT	5585
		AGTTCTATGAGAATTCTAAGTGAAAATAGAGAATTCAAACAAAATG GGTTCTT <del>GGAA</del> TT <del>CA</del> ACAAAAATGCTGAATATGAAGAAGAAACTGA AGTCGAAA <del>ACT</del> CATAGCAGATATGGAA	5586
		TTTTGTGAA <del>TT</del> CCAA	5587
		TTGGAA <del>TT</del> CA <del>CA</del> AAAAA	5588
10	White leaves Immutans <i>Oryza sativa</i> Glu22Term GAG-TAG	TCGGCACGAGGGAGAAGGAGCAGACCGAGGTGGCCGTGAGG AGTCCTTCCCCTTCAGGTAGACGGCTCCTGACGAGCCACTGG TCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCG	5589
		CGAGCTTAACCACCCAGCTCTCCTCGGCCGTGACCAGTGGCTCG TCAGGAGGGAGCCGT <del>T</del> ACCTGAAGGGGAAGGACTCCTCGACGGC CACCTCGGTCTGCTCCTCTCCCTCGTGGCAA	5590
		CCTCAGGTAGACGGCT	5591
		AGCCGTCT <del>AC</del> CTGAAGG	5592
		GAGCAGACCGAGGTGGCCGTGAGGAGTCCTCCCTCAGGGA GACGGCTCCTCCTGACTAGCCACTGGTACCGCCGAGGAGAGCT GGGTGGTTAAGCTCGAGCAGTCCGTGAACATTT	5593
15	White leaves Immutans <i>Oryza sativa</i> Glu28Term CAG-TAG	AAATGTTACGGACTGTCGAGCTTAACCACCCAGCTCCTCGG CGGTGACCAGTGGCT <del>A</del> GT <del>C</del> AGGAGGAGCCGTCCCTGAAGGGG AAGGACTCCTCGACGCCACCTCGGTCTGCTC	5594
		CTCCTGACTAGCCACTG	5595
		CAGTGGCT <del>A</del> GT <del>C</del> AGGAG	5596
		GTCGAGGAGTCCTCCCTTCAGGGAGACGGCTCCTGACGA GCCACTGGTCACCGCCTAGGAGAGCTGGGTGGTTAAGCTCGAGC AGTCGTGAACAT <del>TTT</del> CCTCACGGAGTCAGTCA	5597
20	White leaves Immutans <i>Oryza sativa</i> Glu34Term GAG-TAG	TGACTGACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCTAA CCACCCAGCTCCT <del>A</del> GGCGGTGACCAGTGGCTCGTCAGGAGGA GCCGTCTCCCTGAAGGGGAAGGACTCCTCGAC	5598
		TCACCGCC <del>T</del> AGGAGAGC	5599
		GCTCTCCT <del>A</del> GGCGGTGA	5600
		GAGGAGTCCTCCCTTCAGGGAGACGGCTCCTGACGAGCC ACTGGTCACCGCCGAGTAGAGCTGGGTGGTTAAGCTCGAGCACT CCGTGAACAT <del>TTT</del> CCTCACGGAGTCAGTCATCA	5601
		TGATGACTGACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCT TAACCACCCAGCT <del>T</del> ACTCGGCCGTGACCAGTGGCTCGTCAGGA GGAGCCGTCTCCCTGAAGGGGAAGGACTCCTC	5602
25	White leaves Immutans <i>Oryza sativa</i> Glu35Term GAG-TAG	CCGCCGAG <del>T</del> AGAGCTGG	5603
		CCAGCTCT <del>A</del> CTCGGCCG	5604

5	White leaves Immutans <i>Oryza sativa</i> Trp37Term TGG-TGA	CTTCCCCCTTCAGGGAGACGGCTCCTCCTGACGAGGCCACTGGTCAC CGCCGAGGAGAGCTGAGTGGTTAAGCTCGAGCAGTCCGTGAACA TTTCCTCACGGAGTCAGTCATCACGATACTT	5605
		AAGTATCGTGATGACTGACTCCGTGAGGAAAATGTTCACGGACTG CTCGAGCTTAACCACTCAGCTCCTCGGCGGTGACCAGTGGCTC GTCAGGAGGAGCCGTCCCTGAAGGGGAAG	5606
		GAGAGCTGAGTGGTTAA	5607
		TTAACCACTCAGCTCTC	5608
		TCGGAGGAGGAAGGGGGATTGACGAGGAGCTCACCTCGCCGGCGAGG GCGAGGACGGCGACTGAGTCGTCACTCGAGCAGTCCCTCAAC GTATTCTCACGGATACTGTCATCTTATACTC	5609
10	White leaves Immutans <i>Triticum aestivum</i> Trp22Term TGG-TGA	GAGTATAAAGATGACAGTATCCGTGAGGAATAACGTTGAAGGACTG CTCGAATCTGACGACTCAGTCGCCGTCCCTGCCGGCGAGGGTGA GCTCTCGTCGAATCCCCCTCCTCCCTCGGA	5610
		GGCGACTGAGTCGTAG	5611
		CTGACGACTCAGTCGCC	5612
		GAGGAAGGGGGATTGACGAGGAGCTCACCTCGCCGGCGAGG ACGGCGACTGGTCGTCTGATTGAGCAGTCCTCAACGTATTCC TCACGGATACTGTCATCTTATACTCGATATT	5613
		GAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATAACGTTGAA GGACTGCTCGAATCAGACGACCCAGTCGCCGTCCCTGCCGGCGA GGGTGAGCTCCTCGTCGAATCCCCCTCCTC	5614
15	White leaves Immutans <i>Triticum aestivum</i> Arg25Term AGA-TGA	GGGTGAGCTCTGATTGAG	5615
		CTCGAATCAGACGACCC	5616
		GGGGGATTGACGAGGAGCTCACCTCGCCGGCGAGGACGGCG ACTGGGTGTCAGATTCTAGCAGTCCTCAACGTATTCTCACGGA TACTGTCATCTTATACTCGATATTCTGTATC	5617
		GATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATA GTTGAAGGACTGCTAGAATCTGACGACCCAGTCGCCGTCCCTGCC GGCGAGGGTGAGCTCCTCGTCGAATCCCC	5618
		TCAGATTCTAGCAGTCC	5619
20	White leaves Immutans <i>Triticum aestivum</i> Glu27Term GAG-TAG	GGACTGCTAGAATCTGA	5620
		GGATTCGACGAGGAGCTCACCTCGCCGGCGAGGACGGCGACTG GGTCGTCACTGAGTAGTCCTCAACGTATTCTCACGGATACT GTCATCTTATACTCGATATTCTGTATCGT	5621
		CACGATAACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAA TACGTTGAAGGACTACTCGAATCTGACGACCCAGTCGCCGTCCCTC GCCGGCGAGGGTGAGCTCCTCGTCGAATCC	5622
		GATTGAGTAGTCCTC	5623
		GAAGGACTACTCGAAC	5624
25	White leaves Immutans <i>Triticum aestivum</i> Gln28Term CAG-TAG		

5	White leaves	CGAGCAGTCCTCAACGTATTCTCACGGATACTGTCATCTTATA	5625
	Immutans	CTCGATATTCTGT <u>AGCGT</u> GACCGCGACTACGCAAGGTTCTCGTG	
	<i>Triticum aestivum</i>	CTCGAGACCATGCCAGGGTGCCCTATTTC	
	Tyr46Term	GAAATAGGGCACCCCTGGCGATGGTCTCGAGCACGAAGAACCTTG	5626
	TAT-TAG	CGTAGTCGCGGT <u>CACGCT</u> ACAGAAATATCGAGTATAAAGATGACAG TATCCGTGAGGAATACGTTGAAGGACTGCTCG ATTCTGT <u>AGCGT</u> GACCG	5627
		CGGT <u>CACGCT</u> ACAGAAAT	5628

**Example 9****Altering amino acid content of plants**

Another aim of biotechnology is to generate plants, especially crop plants, with added value traits. An example of such a trait is improved nutritional quality in food crops. For example, lysine, 5 tryptophan and threonine, which are essential amino acids in the diet of humans and many animals, are limiting nutrients in most cereal crops. Consequently, grain-based diets, such as those based on corn, barley, wheat, rice, maize, millet, sorghum, and the like, must be supplemented with more expensive synthetic amino acids or amino-acid-containing oilseed protein meals. Increasing the lysine content of these grains or of any of the feed component crops would result in significant added value.

10 Naturally occurring mutants of plants that have different levels of particular essential amino acids have been identified. However, these mutants are generally not the result of increased free amino acid, but are instead the result of shifts in the overall protein profile of the grain. For example, in maize, reduced levels of lysine-deficient endosperm proteins (prolamines) are complemented by elevated levels of more lysine-rich proteins (albumins, globulins and glutelins). While nutritionally superior, these mutants are 15 associated with reduced yields and poor grain quality, limiting their agronomic usefulness.

An alternative approach is to generate plants with mutations that render key amino acid biosynthetic enzymes insensitive to feedback inhibition. Many such mutations are known and mutation results in increased free amino acid. The increased production can optionally be coupled to increased expression of an abundant storage protein comprising the chosen amino acid. Alternatively, a normally 20 abundant protein can be engineered to contain more of the target amino acid.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that remove feedback inhibition in plant amino acid biosynthetic enzymes.

**Table 19**  
**Genome-Altering Oligos Conferring Amino Acid Overproduction**

	<b>Phenotype, Gene, Plant &amp; Targeted Alteration</b>	<b>Altering Oligos</b>	<b>SEQ ID NO:</b>
5	Met Overproduction CGS <i>Arabidopsis thaliana</i> Arg77His CGT-CAT	TATCCTCCAGGATCTAAGATTCTCCTAATTCTGCCGTAGCT GAGCATTAAAGCCC <u>A</u> TAGAAACTGTAGCAACATCGGTGTTGCACA GATCGTGGCGGCTAAGTGGTCCAACAAACCC	5629
		GGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGAT GTTGCTACAGTTCT <u>A</u> GGGCTTAATGCTCAGCTGACGGACGAA ATTAGGAGGAAATCTAAGATCCTGGAGGATA	5630
		TAAAGCCC <u>A</u> TAGAAACT	5631
		AGTTTCT <u>A</u> GGGCTTA	5632
10	Met Overproduction CGS <i>Arabidopsis thaliana</i> Ser81Asn AGC-AAC	TCTTAAGATTTCTCCTAATTCTGCCGTAGCTGAGCATTAAAGC CCGTAGAAACTGT <u>A</u> CAACATCGGTGTTGCACAGATCGTGGCGG CTAAGTGGTCCAACAACCCATCCTCCCGCGTT	5633
		AACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTG TGCAACACCGATGTTG <u>T</u> ACAGTTCTACGGGCTTAATGCTCAGC TGACGGACGAAATTAGGAGGAAATCTAAGA	5634
		AAACTGT <u>A</u> CAACATCG	5635
		CGATGTTG <u>T</u> ACAGTT	5636
		TTCCCTCCTAATTCTGCCGTAGCTGAGCATTAAAGCCC <u>T</u> AGAA ACTGTAGCAACATC <u>A</u> GTGTTGCACAGATCGTGGCGGCTAAGTGGT CCAACAACCCATCCTCCCGCGTTACCTTCGG	5637
15	Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Ser GGT-AGT	CCGAAGGTAAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCC ACGATCTGTGCAACACT <u>G</u> ATGTTGCTACAGTTCTACGGGCTTAA TGCTCAGCTGACGGACGAAATTAGGAGGAA	5638
		GCAACATC <u>A</u> GTGTTGCA	5639
		TGCAACACT <u>G</u> ATGTTGC	5640
		TTCCCTCCTAATTCTGCCGTAGCTGAGCATTAAAGCCC <u>T</u> AGAAA CTGTAGCAACATC <u>G</u> ATGTTGCACAGATCGTGGCGGCTAAGTGGTC CAACAAACCCATCCTCCCGCGTTACCTTCGGC	5641
		GCCGAAGGTAAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGC CACGATCTGTGCAACAT <u>C</u> GATGTTGCTACAGTTCTACGGGCTTAA ATGCTCAGCTGACGGACGAAATTAGGAGGAA	5642
20	Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Asp GGT-GAT	CAACATC <u>G</u> ATGTTGCAC	5643
		GTGCAACATCGATGTTG	5644
25	Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Asp GGT-GAT		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Met Overproduction CGS <i>Fragaria vesca</i> Arg73His CGC-CAC	TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGC TCAGCACCAAGGCC <u>A</u> CCGCAACTGCAGCAACATCGCGTCGCG CAGATCGTCGCGGCTTGTGGTCCAACAAAGA	5645
		TCTTTGTTGGACCACGAAGCCCGACGATCTGCGCGACGCCGAT GTTGCTGCAGTTGCGGT <u>T</u> GGCCTTGGTGTGAGCTGGCGGACGA AGTTGGGAGGGAAAGCGGAGGATGAGTGACGATA	5646
		CAAGGCC <u>A</u> CCGCAACT	5647
		AGTTGCGGTGGCCTTG	5648
10	Met Overproduction CGS <i>Fragaria vesca</i> Ser77Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAG GCCCGCCGCAACTGCA <u>A</u> CAACATCGCGTCGCGACGATCGTCG GGCTTCGTTGCAACAAAGACTCCGACCTTCGGCGGT	5649
		GAAAGGTGGAGTCTTGTGACCAACGAAGCCCGACGATCTG CGCGACGCCGATGTTG <u>T</u> GCAGTTGCGCGGGCCTTGGTGTGA GCTGGCGACGAAGTTGGGAGGGAAAGCGGAGGA	5650
		CAACTGCA <u>A</u> CAACATCG	5651
		CGATGTTG <u>T</u> GCAGTTG	5652
		TTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG CAACTGCAACAT <u>C</u> AGCGTCGCGCAGATCGTCGCGGCTTCGT GGTCCAACAAAGACTCCGACCTTCGGCGGT	5653
15	Met Overproduction CGS <i>Fragaria vesca</i> Gly80Ser GGC-AGC	GCACCGCCGAAAGGTGGAGTCTTGTGACCAACGAAGCCCG ACGATCTGCGCGACGCT <u>G</u> ATGTTGCTGCAGTTGCGGGGGCCTT GGTGTGAGCTGGCGACGAAGTTGGGAGGGAA	5654
		GCAACAT <u>C</u> AGCGTCGCG	5655
		CGCGACGC <u>T</u> GTGTTG	5656
		TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG AACTGCAACAT <u>C</u> AGCGTCGCGCAGATCGTCGCGGCTTCGT GTCCAACAAAGACTCCGACCTTCGGCGGT	5657
		GGCACCGCCGAAAGGTGGAGTCTTGTGACCAACGAAGCCCG GACGATCTGCGCGACG <u>T</u> CGATGTTGCTGCAGTTGCGGGGGCCT TGGTGTGAGCTGGCGACGAAGTTGGGAGGGAA	5658
20	Met Overproduction CGS <i>Fragaria vesca</i> Gly80Asp GGC-GAC	CAACAT <u>C</u> AGCGTCGCG GCGCGACG <u>T</u> CGATGTTG	5659 5660
		TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCAGGCCAGC TAAGCACCAAGGC <u>G</u> AGGCCAACTGCAGCAACATCGCGTCGCG CAAATCGTCGCCGCTTGTGGTCAACAAACAG	5661
		CTGTTGTCGACCAACGAAGCGCGACGATTTGCAGCGACGCCGAT GTTGCTGCAGTTGCGGCT <u>C</u> GCCTTGGTGTAGCTGGCGCTGGA AGTTGGGAGGGAAAGCGGAGGATGAGGGAGGAGA	5662
		CCAAGGCC <u>G</u> AGCCGCAAC	5663

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTGCGGCTCGCCTTGG	5664
5 Met Overproduction CGS <i>Glycine max</i> Ser72Asn AGC-AAC	TCCTCCGCTCCCTCCCAACTTCCAGCGCCAGCTAACGCACCAAG GCGCGCCGCAACTGCA <u>ACAACATCGGCGTCGCGCAAATCGTCGC</u> CGCTTCGTGGTCGAACAACAGCGACA <u>ACTCTCC</u>	5665
	GGAGAGTTGTCGCTTGTGACCA <u>CGAAGCGGCAGCATTG</u> CGCGACGCCGATGTTG <u>TGCAAGTGCAGTCGGCGCGCCTGGTGCTTA</u> GCTGGCGCTGGAA <u>AGTTGGGAGGGAAAGCGGAGGA</u>	5666
	CAACTGCA <u>ACAACATCG</u>	5667
	CGATGTT <u>TGCAAGTGTG</u>	5668
10 Met Overproduction CGS <i>Glycine max</i> Gly75Ser GGC-AGC	TTCCCTCCCAACTTCCAGCGCCAGCTAACGCACCAAGGC <u>CGCGCCG</u> CAACTGCA <u>ACACATCGCGTCGCGCAAATCGTCGCCGCTTCGT</u> GGTCGAACA <u>ACAGCGACA</u> ACTCTCCGGCCGCG	5669
	CGGCGGCCGGAGAG <u>TTGTCGCTTGTGACCA</u> CGAAGCGGC GACGATTGCGC <u>ACGCTGATGTTGCTGCAGTTGCGGCGCCT</u> TGGTGCTTAG <u>CTGGCGCTGGAAAGTTGGGAGGGAA</u>	5670
	GCAACAT <u>CGCGTCGCG</u>	5671
	CGCGAC <u>CGCTGATGTTG</u>	5672
	TCCCTCCCAACTTCCAGCGCCAGCTAACGCACCAAGGC <u>CGCGCCG</u> AACTGCA <u>ACACATCGACGTCGCGCAAATCGTCGCCGCTTCGT</u> GTCGAACA <u>ACAGCGACA</u> ACTCTCCGGCCGCG	5673
15 Met Overproduction CGS <i>Glycine max</i> Gly75Asp GGC-GAC	CGGCGGCCGGAGAG <u>TTGTCGCTTGTGACCA</u> CGAAGCGGC GACGATTGCGC <u>ACGCTGATGTTGCTGCAGTTGCGGCGCCT</u> TGGTGCTTAG <u>CTGGCGCTGGAAAGTTGGGAGGGAA</u>	5674
	CAACAT <u>CGACGTCGCG</u>	5675
	CGCGAC <u>CGCTGATGTTG</u>	5676
	TGTCTTCTGAT <u>TTCA</u> GGTTCCCTCTAATT <u>CGTGAGGCAGCT</u> .AAGCATTAA <u>AGGCTCACAGGAATTGCA</u> GAATATTGGCGTGGCTCA AGTTGTGGCG <u>CTTCTGGTCAACAA</u> CCA	5677
	TGGTTGTTAGACC <u>AGGAAAGCCGCCACA</u> ACTTGAGCCACGCCAATA TTGCTGCAATT <u>CCTGTGAGCCTTA</u> ATGCTAGCTGCC <u>TCACGAAAT</u> TAGGAGGAAC <u>CTGAAATCAGAGAAGACA</u>	5678
20 Met Overproduction CGS <i>Solanum tuberosum</i> Arg70His AGG-CAC	TAAGG <u>CTCACAGGAATT</u>	5679
	AATT <u>CCCTGTGAGCCTTA</u>	5680
	TTTCAGG <u>TTCCCTCTAATT</u> CGTGAGGCAGCTAAC <u>GTAAAGC</u> TAGGAGGAATT <u>GCAACAAT</u> ATTGGCG <u>GGCTCAAGTTGCGG</u> CTTC <u>CTGGTCAACAA</u> CCAAGCCGG <u>CTCTGA</u>	5681
	TCAGGAC <u>CCGGTTGGTTGTTAGACCAGGAAGCCGCCACA</u> ACTTG AGCCACGCCA <u>ATATTG</u> <u>TGCAATT</u> CCCTAGC <u>CTTAATGCTTAGC</u> TGC <u>CTCACGAAATTAGGAGGAACCTGAAAA</u>	5682
25		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GAATTGCAACAATATTG	5683
	CAATATTG <del>T</del> GCAATTG	5684
5 Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Ser GGC-AGC	TTCCCTCTAATTCGTGAGGCAGCTAACGATTAAGGCTAGGAGG AATTGCAGCAATATT <del>A</del> CGTGGCTAACGTTGTGGCGGCTTCCTGG TCTAACAAACCAAGCCGGCTCTGAATTCACTC	5685
	GAGTGAATTCAAGGACCGGCTTGGTTAGACCAGGAAGCCGC ACAACTTGAGCCACG <del>C</del> TAATATTGCTGCAATTCTCCTAGCCTAA	5686
	TGCTTAGCTGCCTACGAAATTAGGAGGAA	
	GCAATATT <del>A</del> CGTGGCT	5687
	AGCCACG <del>C</del> TAATATTG <del>C</del>	5688
10 Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Asp GGC-GAC	TTCCCTCTAATTCGTGAGGCAGCTAACGATTAAGGCTAGGAGGA ATTGCAGCAATATT <del>G</del> ACGTGGCTAACGTTGTGGCGGCTTCCTGG CTAACAAACCAAGCCGGCTCTGAATTCACTC	5689
	GGAGTGAATTCAAGGACCGGCTTGGTTAGACCAGGAAGCCGC CACAACTTGAGCCACG <del>T</del> CAATATTGCTGCAATTCTCCTAGCCTA	5690
	ATGCTTAGCTGCCTACGAAATTAGGAGGAA	
	CAATATTG <del>A</del> CGTGGCT	5691
	GAGCCACG <del>T</del> CAATATTG <del>C</del>	5692
15 Met Overproduction CGS <i>Mesembryanthemum</i> <i>crystallinum</i> Arg73His CGC-CAC	CTTCCTCTTATCCCTCGCTTCCCTCCAACTTTGTCCGTCAAGCT CAGCACCAAGGCTGCC <del>A</del> CAACTGCAACATTGGTGTGCCAC AGGTCTCGCTGCCCTGGTCCAACAACTC	5693
	GAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACCAAT GTTGCTGCAGTTG <del>T</del> GGCGAGCCTGGTCTGAGCTGACGGACAA	5694
	AGTTGGGAGGAAGCGAAGGATAAGAGAGAGGAAG	
	GGCTCGCC <del>A</del> CAACTGCA	5695
	TGCAGTTG <del>T</del> GGCGAGCC	5696
20 Met Overproduction CGS <i>Mesembryanthemum</i> <i>crystallinum</i> Ser77Asn AGC-AAC	TCCCTCGCTTCCCTCCAACTTTGTCCGTCAAGCTCAGCACCAAGG CTCGCCGCAACTGCA <del>A</del> CAACATTGGTGTGCACAGGTCTCGCT GCCCTCTGGTCCAACAACTCCGATGCCGGCGC	5697
	GCGCCGGCATGGAGTTGGACCAGGAGGCAGCGACGACCT GTGCGACACCAATGTTG <del>T</del> GCAGTTGCGGGAGCCTGGTCTG AGCTGACGGACAAAGTTGGGAGGAAGCGAAGGA	5698
	CAACTGCAACACATTG <del>C</del>	5699
	CAATGTTG <del>T</del> GCAGTTG <del>C</del>	5700

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Met Overproduction CGS <i>Mesembryanthemum</i> <i>crystallinum</i> Gly80Ser GGT-AGT	TTTCCTCCCAACTTTGTCGTCAGCTCAGCACCAAGGCTGCCGC AACTGCAGCAACATT <u>A</u> GTGTCGCACAGGTCGTCGCTGCCCTTG GTCCAACAACCTCGATGCCGGGCCACCTCTT	5701
	AAGAGGTGGCGCCGGCATCGGAGTTGGACCAGGAGGCAGC GACGACCTGTGCGACACTAATGTTGCTGCAGTTGGGGAGCCT TGGTGCTGAGCTGACGGACAAAGTTGGGAGGAAA	5702
	GCAACATT <u>A</u> GTGTCGCA	5703
	TGGGACACTAATGTTGC	5704
	TTTCCTCCCAACTTTGTCGTCAGCTCAGCACCAAGGCTGCCGCA ACTGCAGCAACATT <u>G</u> ATGTCGCACAGGTCGTCGCTGCCCTTG TCCAACAACCTCGATGCCGGGCCACCTCTT CAAGAGGTGGCGCCGGCATCGGAGTTGGACCAGGAGGCAG CGACGACCTGTGCGACATCAATGTTGCTGCAGTTGGCGAGCC TGGTGCTGAGCTGACGGACAAAGTTGGGAGGAA	5705 5706
10 Met Overproduction CGS <i>Mesembryanthemum</i> <i>crystallinum</i> Gly80Asp GGT-GAT	CAACATT <u>G</u> ATGTCGAC	5707
	GTGCGACAC <u>A</u> CAATGTTG	5708
	CCTCTGCTACCATCCCTCGCTTCCGCCAAACTTTGTCGCCAGC TTAGCACCAAGGCAC <u>A</u> CCGCAACTGCAGCAACATGGCGTCGCG CAGATCGTCGCCGCGCGTGGTCCGACTGCC GGGCAGTCGGACCACGCCGGCGACGATCTGCCGACGCCGA TGTTGCTGCAGTTGGG <u>T</u> GTGCCCTGGTCTAAGCTGGCGACA AAGTTGGCGAAAGCGGAGGATGGTAGCAGAGG	5709 5710
	CAAGGCAC <u>A</u> CCGCAACT	5711
	AGTTGCGG <u>T</u> GTGCCCTTG	5712
15 Met Overproduction CGS <i>Zea mays</i> Arg41His CGC-CAC	TCCTCCGCTTCCGCCAAACTTTGTCGCCAGCTAGCACCAAGG CACGCCGCAACTGC <u>A</u> CAACATCGCGCGCAGATCGTCGCC	5713
	GCCCGCGTGGTCCGACTGCCCGCCGCTGCC GGGCAGCGGCGGGGCAGTCGGACCACGCCGGCGACGATC	5714
	TGCGCGACGCCGATGTTG <u>T</u> GCAGTTGGCGCTGCCCTGGTCT AAGCTGGCGAACAAAGTTGGCGAAAGCGGAGGA	
	CAACTGCA <u>A</u> CAACATCG	5715
	CGATGTTG <u>T</u> GCAGTTG	5716
20 Met Overproduction CGS <i>Zea mays</i> Ser45Asn AGC-AAC	TTTCGCCAAACTTTGTCGCCAGCTAGCACCAAGGCACGCCGC AACTGCAGCAACAT <u>C</u> AGCGTCGCGCAGATCGTCGCCGCCGTG GTCGACTGCCCGCCGCTGCCCTTTACTTAG	5717
	CTAAGTGGGGCGAGCGGCGGGCAGTCGGACCACGCCGG CGACGATCTGCGCGACGCT <u>G</u> ATGTTGCTGCAGTTGGCGTGCC TGGTGCTAACAGCTGGCGAACAAAGTTGGCGGAAA GCAACAT <u>C</u> AGCGTCGCG	5718 5719

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Met Overproduction CGS <i>Zea mays</i> Gly48Asp GGC-GAC	CGCGACGCTGATGTTGC	5720
		TTCCGCCAAACTTGTCCGCCAGCTTAGCACCAAGGCACGCCGC AACTGCAGCAACATCG <u>A</u> CGTCCGCGAGATCGTCGCCGCCGCGT GTCCGACTGCCCCGCCGCTCGCCCCACTTAGG	5721
		CCTAAGTGGGGCGAGCGGGGGGAGTCGGACCGACGCCG GCGACGATCTGCGCGACG <u>T</u> CGATGTTGCTGCAGTTGCCGCGTGC CTTGGTCTAAGCTGGCGGACAAAGTTGGCGAA	5722
		CAACATCG <u>A</u> CGTCCGCG GCGCGACG <u>T</u> CGATGTTG	5723 5724
		GTATGAATGATCTGTGGGTGAAACACTGTGGGATTAGTCATA GAAGTTCAAGGATCG <u>T</u> GAATGACTGTTGGTAGTCAGTTAA TCGTCTGAGAAAGATGAAACGACCTGTGGT	5725
10	Met Overproduction TS <i>Arabidopsis thaliana</i> Leu205Arg CTT-CGT	ACCACAGGTCGTTCATCTTCTCAGACGATTAAC AAACAGTCATTCCACG <u>A</u> CTCCTGAAACTCCCTGTATGACTAACCA ACAGTGTTCACCCACAGATCATTAC	5726
		CAAGGATCG <u>T</u> GGAAATGA	5727
		TCATTCCACG <u>A</u> CTCCTG	5728
		GCATGACTGATTTGTGGGCAAACACTGTGGGATTAGCCATA GTAGTTAAGGATCG <u>T</u> GGGATGACTGTTGGTAGTCAGTTAA TCGCTTGCGGAAAATGCATAAACCGGGTT	5729
		ACAACCGGTTATGCATTTCCGCAAGCGATTAAC AAACAGTCATCCCACG <u>A</u> CTCCTAAA ACAGTGTTCACCCACAAATCAGTCATGC	5730
15	Met Overproduction TS <i>Solanum tuberosum</i> Leu198Arg CTT-CGT	TAAGGATCG <u>T</u> GGGATGA	5731
		TCATCCCACG <u>A</u> TCCTTA	5732
		TCATTGGGCACACAGTGA TAGGCAACACAGGAA <u>A</u> CAACTCAACCAGAGAAGCCGTCCACGCA ACAGAACAGGGATTGCTGTTGGCATGCATGC	5733
		GCATGCATGCCAACAGCAAATCCCTGTTCTGTTGGACGGCT TCTCTGGTTGAGTTG <u>T</u> TCCTGTGTTGCCATCACTTGATTCTAG AGCCAAAGCAGTTCACTGTGTGCCAATGA	5734
		CACAGGAA <u>A</u> CAACTCAA	5735
20	Lys Overproduction DHPS <i>Zea mays</i> Ser157Asn AGC-AAC	TTGAGTTG <u>T</u> TCCTGTG	5736
		GCTCTAGAATCAAAGTGA GAGAACCGTCCACG <u>A</u> ACAGAACAGGGATTGCTGTTGGCATG CATGCCGTCTCCACATCAATCCTACTACGG	5737
		CCGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGC AAATCCCTGTTCTGTT <u>T</u> CGTGGACGGCTCTGGTTGAGTTGCTT CCTGTGTTGCCATCACTTGATTCTAGAGC	5738
25	Lys Overproduction DHPS <i>Zea mays</i> Ala166Val GCA-GAA		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGTCCACG <u>A</u> ACAGAAC GTTCTG <u>T</u> CGTGGACG	5739 5740
5 Lys Overproduction DHPS <i>Zea mays</i> Ala166Thr GCA-ACA	GGCTCTAGAACAGTGTAGGCAACACAGGAAGCAACTCAACC AGAGAACGCCGTCCAC <u>A</u> CAACAGAACAGGGATTGCTGTTGGCAT GCATGCGGCTCTCCACATCAATCCTTACTACG CGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCAA ATCCCTGTTCTGTT <u>G</u> TGGACGGCTCTGGTTGAGTTGCTTC CTGTGTTGCCTATCACTTGATTCTAGAGCC CCGTCCAC <u>A</u> CAACAGAA TTCTGTTG <u>T</u> GTTGGACGG	5741 5742 5743 5744
10 Lys Overproduction DHPS <i>Oryza sativa</i> Ser124Asn AGT-AAT	TTATTGGGCATACAG <u>T</u> AACTGCTTGCACTAAATAAAGTGGT CGGCAACACAGGA <u>A</u> TA <u>T</u> ACTCAACAAAGGGAGGCTATTACGCAAC TGAGCAGGGATT <u>C</u> GCTGTAGGTATGCACGC GCGTGCATACCTACAG <u>C</u> GAATCCCTGCTCAGTTGCGTGAATAGCC TCCCTGTTGAGTT <u>A</u> TTCCCTGTTGCCGACC <u>A</u> CTTTAATTTAGT GCCAAAGCAGTT <u>A</u> CTGTATGCCAATAA CACAGGA <u>A</u> TA <u>T</u> ACTCAA TTGAGTT <u>A</u> TTCCCTG <u>G</u>	5745 5746 5747 5748
15 Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Val GCA-GTA	GCACTAAAATAAAGTGGCGCAACACAGGAAGTA <u>T</u> CAACAA GGGAGGCTATT <u>C</u> AC <u>T</u> AACTGAGCAGGGATT <u>C</u> GCTGTAGGTATG CACGCGGCTCTCCACATCAATCCTTACTACGG CCGTAGTAAGGATTGATGTGGAGAGCCCGTGCATACCTACAGC GAATCCCTGCTCAGTT <u>A</u> CGTGAATAGCC <u>C</u> CC <u>T</u> TTGTTGAGTTACTT CCTGTGTTGCCGACC <u>A</u> CTTTAATTTAGTGC TATT <u>C</u> AC <u>G</u> TAA <u>T</u> GAGC GCTCAGTT <u>A</u> CGTGAATA	5749 5750 5751 5752
20 Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Thr GCA-ACA	GGCACTAAAATAAAGTGGCGCAACACAGGAAGTA <u>T</u> CAACAA AGGGAGGCTATT <u>C</u> AC <u>A</u> ACTGAGCAGGGATT <u>C</u> GCTGTAGGTAT GCACGCGGCTCTCCACATCAATCCTTACTACG CGTAGTAAGGATTGATGTGGAGAGCCCGTGCATACCTACAGC AATCCCTGCTCAGTT <u>G</u> TGAATAGCC <u>C</u> CC <u>T</u> TTGTTGAGTTACTC CTGTGTTGCCGACC <u>A</u> CTTTAATTTAGTGC CTATT <u>C</u> AC <u>A</u> ACTGAG CTCAGTT <u>G</u> TGAATA	5753 5754 5755 5756
25 Lys Overproduction DHPS 1 <i>Triticum aestivum</i>	TCATCGGGCATA <u>T</u> GTTAACTGCTTGAG <u>C</u> CAAC <u>A</u> TTAAAGTGA <u>T</u> AGGCAACAC <u>GGG</u> <u>A</u> TA <u>T</u> ACTCAAC <u>C</u> CC <u>A</u> GAG <u>A</u> AG <u>C</u> TGTT <u>C</u> AC <u>CG</u> <u>G</u> CAGAGCAGGGATTGCTGTTGGCATGCATGC	5757
Ser165Asn AGT-AAT		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GCATGCATGCCAACAGCAAATCCCTGCTCTGCGCGTGAACAGCTCTCTGGTGTAGTTA <del>TT</del> CCCGTGTGCCATCACTTAATGTTGGCTCCAAAGCAGTTAACAGTATGCCGATGACACGGGAA <del>AA</del> TAACCTCAA	5758
	TTGAGTTA <del>TT</del> CCCGTGT	5759
		5760
5 Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Val GCG-GTG	GAGCCAACATTAAAGTGTAGGCAACACGGGAAGTAACCTAACCA GAGAAGCTGTTCACGTGACAGAGCAGGGATTGCTGTTGGCATGCATGCAGCTCTCATGTCAATCCTACTACGG	5761
	CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTCA <del>AC</del> GTGAACAGCTCTCTGGTTGAGTTACTT CCCGTGTGCCTATCACTTAATGTTGGCTC	5762
	TGTTCACGTGACAGAGC	5763
	GCTCTGTCA <del>AC</del> GTGAACA	5764
10 Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Thr GCG-ACG	GGAGCCAACATTAAAGTGTAGGCAACACGGGAAGTAACCTAACCA AGAGAAGCTGTTCAC <del>AC</del> GTGACAGAGCAGGGATTGCTGTTGGCATGCATGCAGCTCTCATGTCAATCCTACTACG	5765
	CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTGTC <del>GT</del> GAACAGCTCTCTGGTTGAGTTACTTC CCGTGTGCCTATCACTTAATGTTGGCTC	5766
	CTGTTCAC <del>AC</del> GTGACAGAG	5767
	CTCTGTGTC <del>GT</del> GAACAG	5768
15 Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ser154Asn AGT-AAT	TCATGGGCACACTGTTAACTGCTTGGAACTAACATTAAAGTGTAGGCAACACGGGA <del>AA</del> TAACCTAACCA AGAGCAGGGATTGCTGTTGGCATGCATGCAGCAGGGATTGCTGTTGGCATGCATGC	5769
	GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCTCTCTAGTTA <del>TT</del> CCCGTGTGCCATCACTTAATGTTAGTTCCAAAGCAGTTAACAGTGTGCCGATGA	5770
	CACGGGAA <del>AA</del> TAACCTCAA	5771
	TTGAGTTA <del>TT</del> CCCGTGT	5772
20 Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Val GCT-GTT	GAACTAACATTAAAGTGTAGGCAACACGGGAAGTAACCTAACTA GAGAAGCGATTCACG <del>TT</del> CAGAGCAGGGATTGCTGTTGGCATGCATGCAGCTCTCCATGTCAATCCTACTATGG	5773
	CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGAA <del>AC</del> GTGAATCGCTCTAGTTGAGTTACTTC CCGTGTGCCTATCACTTAATGTTAGTT	5774
	GATTCA <del>CG</del> TTCAGAGC	5775
	GCTCTGAA <del>AC</del> GTGAATC	5776

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Thr GCT-ACT	GGAACTAACATTAAAGTGTAGGCAACACGGGAAGTAACACTCACT AGAGAAGCGATTCAC <u>ACT</u> TCAGAGCAGGGATTGCTGTTGGCATG CATGCAGCTCTCCATGTCAATCCTTACTATG	5777
		CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGAAG <u>GT</u> GAATCGCTCTAGTTGAGTTACTTCC CGTGTGCCTATCACTTAATGTTAGTTCC	5778
		CGATTCA <u>AC</u> TTCAGAG	5779
		CTCTGAAG <u>GT</u> GAATCG	5780
10	Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ser154Asn AGT-AAT	CTCAATTGGGCATACTGTGA <u>ACTG</u> CTTGCTCTAGAATTAAAGTGA TAGGCAACACAGGAA <u>ATA</u> ACTCAACCAGAGAAGCTGTTACGC CAGAGCAGGGATTGCTGTTGGCATGCATG	5781
		CATGCATGCCAACAGCAA <u>AT</u> CCCTGCTCTGTTGCGTAACAGCTT CTCTGGTTGAGTT <u>AT</u> TCCTGTGTTGCCTATCACTTAATTCTAGA GCCAAAGCAGTTCACAGTATGCCCAATGAG	5782
		CACAGGAA <u>ATA</u> ACTCAA	5783
		TTGAGTT <u>AT</u> TCCTGTG	5784
15	Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Val GCA-GTA	GCTCTAGAATTAAAGTGTAGGCAACACAGGAAGTAACCAACCA GAGAAGCTGTT <u>ACG</u> TAA <u>AC</u> AGAGCAGGGATTGCTGTTGGCATGC ATGCAGCTCTCCACATCAATCCTTACTATGG	5785
		CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTT <u>ACG</u> TGAACAGCTCTGGTTGAGTTACTTC CTGTGTTGCCTATCACTTAATTCTAGAGC	5786
		TGTTCAC <u>GT</u> AACAGAGC	5787
		GCTCTGTT <u>ACG</u> TGAACA	5788
20	Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Thr GCA-ACA	GGCTCTAGAATTAAAGTGTAGGCAACACAGGAAGTAACCAACCA AGAGAAGCTGTT <u>ACA</u> AC <u>AC</u> AGAGCAGGGATTGCTGTTGGCATG CATGCAGCTCTCCACATCAATCCTTACTATG	5789
		CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTT <u>GT</u> GAACAGCTCTGGTTGAGTTACTTC TGTGTTGCCTATCACTTAATTCTAGAGCC	5790
		CTGTTCAC <u>ACA</u> ACAGAG	5791
		CTCTGTT <u>GT</u> GAACAG	5792
25	Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ser136Asn AGC-AAC	TCATTGGTCACACAGTCATTGTTGGAGGGCCATCAAAGTCAT CGGGAACACTGGAA <u>ACA</u> CTCCACAAGGGAAAGCAATCCATGCAA CTGAACAGGGATTGCTGTAGGTATGCATGC	5793
		GCATGCATACCTACAGCAA <u>AT</u> CCCTGTT <u>GT</u> GAACAGCTCTGGATTGCTT CCCTGTGGAGTT <u>GT</u> CCAGTGTCCCGATGACTTTGATGGACC CTCCAAAACAATTGACTGTGTGACCAATGA	5794
		CACTGGAA <u>ACA</u> CTCCA	5795

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		TGGAGTTG <del>T</del> CCAGTG	5796
5	Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Val GCA-GTA	GAGGGTCCATCAAAGTCATCGGGAACACTTGGAAAGCAACTCCACAA GGGAAGCAATCCATG <del>T</del> A <del>T</del> CTGAACAGGGATTGCTGTAGGTATGC ATGCAGCTTCACATTAATCCCTACTATGG	5797
		CCATAGTAGGGATTAA <del>T</del> GTGAAGAGCTGCATGCATA <del>C</del> CTACAGCA AATCCCTGTT <del>C</del> AGTT <del>A</del> CATGGATTGCTTCC <del>T</del> GTGGAGTTGCTTC CAGTGT <del>T</del> CCGATGACTTTGATGGACCCTC	5798
		AATCCATG <del>T</del> A <del>T</del> CTGAAC	5799
		GTTCAGTT <del>A</del> ATGGATT	5800
10	Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Thr GCA-ACA	GGAGGGTCCATCAAAGTCATCGGGAACACTTGGAAAGCAACTCCAC AAGGGAAAGCAATCCAT <del>A</del> CAACTGAACAGGGATTGCTGTAGGTAT GCATGCAGCTTCACATTAATCCCTACTATG	5801
		CATAGTAGGGATTAA <del>T</del> GTGAAGAGCTGCATGCATA <del>C</del> CTACAGCA ATCCCTGTT <del>C</del> AGTT <del>T</del> ATGGATTGCTTCC <del>T</del> GTGGAGTTGCTTC AGTGT <del>T</del> CCGATGACTTTGATGGACCCTC	5802
		CAATCCAT <del>A</del> CAACTGAA	5803
		TTCAGTTG <del>T</del> ATGGATTG	5804
		TTATAGGCCATACCG <del>T</del> AA <del>T</del> GTTGGCGGAAGCATCAAAGTCAT TGGAAACACTGGAA <del>A</del> CAATTGACTAGAGAAGCAATCCACGCGAC TGAACAAGGATT <del>T</del> CGCGGTTGGAATGCATGC	5805
15	Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ser142Asn AGC-AAC	GCATGCATTCCAACCGCGAATCCTGTT <del>C</del> AGTCGCGTGGATTGCT TCTCTAGTCGAATTG <del>T</del> TCAGTGT <del>T</del> CCAATGACTTTGATGCTTC CGCCAAAACAGTTAACGGTATGGCCTATAA	5806
		CACTGGAA <del>A</del> CAATTGCA	5807
		TCGAATTG <del>T</del> CCAGTG	5808
		GGCGGAAGCATCAAAGTCATTGGAAACACTTGGAAAGCAATTGACTA GAGAAGCAATCCACG <del>T</del> GACTGAACAAGGATT <del>T</del> CGCGGTTGGAATGC	5809
20	Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Val GCG-GTG	ATGCTGCTTCATATAAACCC <del>T</del> ACTATGG CCATAGTAAGGGTTATATGAAGAGCAGCATGCATTCCAACCGCG AATCC <del>T</del> GGTT <del>C</del> AGTC <del>A</del> CGTGGATTGCTTCTAGTCGAATTGCTTC CAGTGT <del>T</del> CCAATGACTTTGATGCTTC <del>G</del> CG	5810
		AATCCACG <del>T</del> GACTGAAC	5811
		GTTCAGTC <del>A</del> CGTGGATT	5812
		GGCGGAAGCATCAAAGTCATTGGAAACACTTGGAAAGCAATTGACT AGAGAAGCAATCCAC <del>A</del> CGACTGAACAAGGATT <del>T</del> CGCGGTTGGAATG CATGCTGCTTCATATAAACCC <del>T</del> ACTATG	5813
25	Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Thr GCG-ACG	CATAGTAAGGGTTATATGAAGAGCAGCATGCATTCCAACCGCGA ATCCTTGTT <del>C</del> AGTC <del>G</del> GTGGATTGCTTCTAGTCGAATTGCTTC AGTGT <del>T</del> CCAATGACTTTGATGCTTC <del>G</del> CG	5814

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAATCCAC <u>AC</u> CGACTGAA	5815
	TTCAGTCG <u>T</u> GTGGATTG	5816
5 Lys Overproduction DHPS <i>Glycine max</i> Ser103Asn AGC-AAC	TTATTGCTCATACAGTCACGTGTTGGTGGGAAAATTAAAGGTATT GGAAATACTGGAA <u>AC</u> AACTCCACCAGGGAGCAATTATGCCACT GAGCAGGGTTTGCTGTTGGAATGCATGC GCATGCATCCAACAGCAA <u>AC</u> CCCTGCTCAGTGGCATGAATTGCT TCCCTGGAGTTG <u>T</u> TCAGTATTCCAATAACCTTAATTTC CACCAAAACAGTTGACTGTATGAGCAATA TACTGGAA <u>AC</u> AACTCCA TGGAGTTG <u>T</u> TCAGTA	5817 5818 5819 5820
10 Lys Overproduction DHPS <i>Glycine max</i> Ala112Val GCC-GTC	GTGGGAAAATTAAAGGTTATTGGAATACTGGAAGCAACTCCACCA GGGAAGCAATTATG <u>T</u> CACTGAGCAGGGTTTGCTGTTGGAATGC ATGCTGCCCTTCACATAACCTTACTATGG CCATAGTAAGGGTTATGTGAAGGGCAGCATGCATTCAAACAGCA AAACCTGCTCAGTG <u>AC</u> ATGAATTGCTTCCCTGGTGGAGTTGCTT CCAGTATTCCAATAACCTTAATTCCCAC AATTCA <u>TG</u> CACTGAGC GCTCAGTG <u>AC</u> ATGAATT	5821 5822 5823 5824
15 Lys Overproduction DHPS <i>Glycine max</i> Ala112Thr GCC-ACC	GGTGGGAAAATTAAAGGTTATTGGAATACTGGAAGCAACTCCACCA AGGGAA <u>GC</u> ATTCA <u>AC</u> CACTGAGCAGGGTTTGCTGTTGGAATG CATGCTGCCCTTCACATAACCTTACTATG CATAGTAAGGGTTATGTGAAGGGCAGCATGCATTCAAACAGCAA AAACCTGCTCAGTG <u>T</u> ATGAATTGCTTCCCTGGTGGAGTTGCTTC CAGTATTCCAATAACCTTAATTCCCAC CAATTCA <u>AC</u> CACTGAG CTCAGTGG <u>T</u> ATGAATTG	5825 5826 5827 5828
20 Trp Overproduction AS <i>Arabidopsis thaliana</i> Asp341Asn GAC-AAC	CTTGCAGGAGACATATTCA <u>GC</u> ATCGTGCTGAGTCACGTTTGAG CGGCGAACATTGCA <u>AC</u> CCCTTGAGTTATAGAGCACTAAGA GTTGTGAATCCA <u>AC</u> GTCCGTATATGGTTATT AATAACCCATATACGGACTTGAGTTCAAACTCTTAGTGCTCTATA AACTCAAAGGGGT <u>T</u> GC <u>AA</u> ATGTTCGCCGCTCAAACGTTGACT CAGCACGATCTGA <u>AA</u> ATATGTCTCCTGCAAG CATTG <u>CA</u> ACCCCTT AAAGGGGT <u>T</u> GC <u>AA</u> ATG	5829 5830 5831 5832
25 Trp Overproduction AS <i>Nicotiana tabacum</i>	GCTGCAGGAGACATATTCA <u>AA</u> ATCGTTAAGTCACGCTTGAGA GAAGAACATTGCA <u>AC</u> CCATTGAAGTGACAGAGCATTAAAGAAT TGTGAATCCA <u>AG</u> CCC <u>AT</u> ATGACTTACA	5833

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TGTAAGTCATATATGGCTGGATTACAATTCTTAATGCTCTGTA CACTTCAAATGGGT <del>T</del> AGCAAATGTTCTCTCAAAGCGTTGACTT AAAACGATTGAAATATGTCTCCTGCAGC	5834
	CATTGCT <del>A</del> ACCCATT	5835
	AAATGGGT <del>T</del> AGCAAATG	5836
5 Trp Overproduction AS <i>Oryza sativa</i> Asp323Asn GAC-AAC	CTAGCTGGTGACATTTCAAGTAGTCTTAAGCCAGCGTTTGAGA GGCGTACATTGCT <del>A</del> ACCCCTTGAGGTGTACCGTGCATTGCGTA TTGTCATCCTAGTCCTTATATGGCCTATC	5837
	GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGT ACACCTCAAGGGGT <del>T</del> AGCAAATGTACGCCCTCTAAAACGCTGGC TTAAGACTACTTGGAAAATGTCACCAAGCTAG	5838
	CATTGCT <del>A</del> ACCCCTT	5839
	AAAGGGGT <del>T</del> AGCAAATG	5840
	CTTGCCTGGTGACATATTCCAGATCGTACTAAGTCAGCGTTTGAAA GGCGAACGTTCGCA <del>A</del> ACCCATTGAAATCTATAGATCACTGAGGA TTGTTAATCCAAGCCCATAATGACTTATT	5841
10 Trp Overproduction AS <i>Ruta graveolens</i> Asp354Asn GAC-AAC	AATAAGTCATATATGGCTGGATTACAATCCTCAGTGATCTATA GATTCAAATGGGT <del>T</del> TGCGAACGTTGCCCTTCAAACGCTGACTT AGTACGATCTGGAATATGTCACCAAGCAAG	5842
	CGTCGCA <del>A</del> ACCCATT	5843
	AAATGGGT <del>T</del> TGCGAACG	5844
	CTGGCTGGGGACATATTCCAGCTGTCTAAGTCAGCGTTTGAA CGGCGAACATTGCA <del>A</del> ATCCATTGAAGTCTACCGAGCATTGAGA ATTGTCAACCCAAGTCCATATATGACTTATT	5845
15 Trp Overproduction AS <i>Catharanthus roseus</i> Asp354Asn GAT-AAT	AATAAGTCATATATGGACTGGGTTGACAATTCTCAATGCTCGGTA GACTTCAAATGGAT <del>T</del> TGCAAATGTTGCCGTTCAAACGCTGACTT AGGACAAGCTGGAATATGTCcccAGCCAG	5846
	CATTGCA <del>A</del> ATCCATT	5847
	AAATGGATTGCAAATG	5848

**Example 10****Production of modified starch in plants**

A principal aim of biotechnology is the improvement of crop plants for food value, agriculture, and to produce a range of plant-derived raw materials. Along with oils, fats and proteins, polysaccharides constitute the main raw materials derived from plants, and apart from cellulose, the storage polymer starch is the most important polysaccharide raw material. Starch is derived from a range of plants, but maize is the most important cultivated plant for the production of starch.

The polysaccharide starch is a polymer made up of glucose molecules. However, starch is not a homogeneous raw material and is, in fact, a highly complex mixture of various types of molecules which differ from each other, for example, in their degree of polymerization and in the degree of branching of the glucose chains. For example, amylose-starch is a basically non-branched polymer made up of  $\alpha$ -1,4-glycosidically branched glucose molecules, and amylopectin-starch is a complex mixture of variously branched glucose chains. The branching results from additional  $\alpha$ -1,6-glycosidic linkages. In plants from which starch is typically isolated, for example maize or potato, the starch is approximately 25% amylose-starch and 75% amylopectin-starch.

In maize, various mutants in starch metabolism are known, for example *waxy*, *sugary*, *shrunken* and *opaque-2*. In addition to producing a modified starch, these mutations greatly improve grain quality in maize, and thus expand the use of maize not only as the food but also for the important industrial materials in food chemistry. It would therefore be advantageous to be able readily to obtain mutants in these genes in particular maize genotypes as well as other plants. Such plants can be obtained, for example, using traditional breeding methods and through specific genetic modification by means of recombinant DNA techniques.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

**Table 20**  
**Genome-Altering Oligos Conferring Increased Starch**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Ala99Lys GCA-AAA	GAACTTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATT ATTCTTGGAGGTGGAA <u>AAAGGA</u> ACTCGACTCTTCCTCTCACAAA CGCCCGGCCAAGCCTGCCGTTCTATCGGGG	5849
		CCCCGATAGGAACGGCAGGCTGGCGCGCGTTTGAGAGGA AAGAGTCGAGTTCTTCCACCTCCAAGAATAATGGAAGCAACT GTCCTTGGATCCCTTCTCAGTCTCAAGTTC	5850
		GAGGTGG <u>AAAGGA</u> ACT	5851
		AGTTCC <u>TTT</u> CCACCTC	5852
10	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro127Leu CCA-CTA	CAAAACGCCGCCAAGCCTGCCGTTCTATCGGGGGAGCCTAT AGG <u>TTG</u> ATAGATGTACT <u>AA</u> TGAGCAATTGTATTAAACAGCGGAATCA ACAAAGTCTACATACTCACACAATATAACTC	5853
		GAGTTATATTGTGAGTATGTAGACTTTGATTCCGCTGTTAA TACAATTGCTCATT <u>AG</u> TACATCTATCAACCTATAGGCTCCCCGAT AGGAACGGCAGGCTGGCGCGCGTTTG	5854
		AGATGT <u>ACT</u> <u>AA</u> TGAGCA	5855
		TGCTCATT <u>AG</u> TACATCT	5856
		TCACACAA <u>TAA</u> CTCAGCATCATTGAACAGGCATTAGCCCGTGC TTACA <u>ACT</u> CCA <u>AA</u> T <u>CTT</u> GGCTTGAGATGGCTATGTTGAGGTT CTTGC <u>GG</u> CC <u>AA</u> CTCAA <u>AC</u> GCC <u>AGG</u> GAGAATC	5857
15	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAT	GATTCTCCTGGCGTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAA <u>AG</u> CCA <u>AG</u> <u>TT</u> ATTGGAGTTGTAAGCACGGCTAAATGC CTGTTCAATGATGCTGAGTTATTTGTGTGA	5858
		CTCCA <u>AA</u> T <u>CTT</u> GGCT	5859
		AGCCA <u>AG</u> <u>TT</u> ATTGGAG	5860
		TCACACAA <u>TAA</u> CTCAGCATCATTGAACAGGCATTAGCCCGTGC TTACA <u>ACT</u> CCA <u>AA</u> <u>AC</u> CTTGGCTTGAGATGGCTATGTTGAGGTT CTTGC <u>GG</u> CC <u>AA</u> CTCAA <u>AC</u> GCC <u>AGG</u> GAGAATC	5861
		GATTCTCCTGGCGTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAA <u>AG</u> CCA <u>AG</u> <u>TT</u> ATTGGAGTTGTAAGCACGGCTAAATGC CTGTTCAATGATGCTGAGTTATTTGTGTGA	5862
20	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAT	CTCCA <u>AA</u> <u>AC</u> CTTGGCT	5863
		AGCCA <u>AG</u> <u>TT</u> ATTGGAG	5864
25	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAC		

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Asn100Lys AAT-AAA	GTTCGAGAGAAGAAAGGTAGACCCGCAAAATGTGGCTGCAATCAT TCTAGGAGGGAGGCAA <u>AGGAGCTAA</u> CTCTCCCTCTTACAATGAG AGCCGCAACACCAGCTGAAATATTCTACCTT	5865
		AAGATGAATATTACAGCTGGTGTGGCTCTATTGTAAGAGG GAAGAGTTAGCTCC <u>TTGCCTCCT</u> AGAATGATTGCAGCCAC ATTTGCGGGTCTACCTTCTCTCTCAAAC	5866
		GGAGGCAA <u>AGGAGCTAA</u>	5867
		TTAGCTCC <u>TTGCCTCC</u>	5868
10	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro128Leu CCG-CTG	CTTGTGTCTCAAATTATGTTAGGTCCTGTTGGTGGATGCTACAG GCTGATCGATATCCT <u>GATGAGTA</u> ACTGTATTAACAGCTGCATCAAC AAGATATTGTGCTGACACAGTCAACTC	5869
		GAGTTGAACTGTGTCAGCACAAATATCTTGTGATGCAGCTGTTAA TACAGTTACTCAT <u>CAGGATATCGATCAGCCTG</u> TAGCATCCACCAA CAGGAACCTAACATAATTGAAAGACACAAG	5870
		CGATATCC <u>GATGAGTA</u>	5871
		TACTCAT <u>CAGGATATCG</u>	5872
		TGACACAGTCAACTCAGCTCCCTTAATCGACATTAGCACCGAAC TTATTTGGAATA <u>ATATAAA</u> CTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5873
15	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAT	GCTGAGAGTTATTATTGTATAGTGTGTTGACCTCTACGAAACCAC CTCCAAAGTTAT <u>ATT</u> ATTCCAAAATAAGTTCGTGTAAATGTCG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	5874
		TGGGAATA <u>ATATAAA</u> CT	5875
		AGTTTAT <u>ATT</u> ATTCCCA	5876
		TGACACAGTCAACTCAGCTCCCTTAATCGACATTAGCACCGAAC TTATTTGGAATA <u>ACATAAA</u> CTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5877
20	Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAC	GCTGAGAGTTATTATTGTATAGTGTGTTGACCTCTACGAAACCAC CTCCAAAGTTAT <u>GTT</u> ATTCCAAAATAAGTTCGTGTAAATGTCG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	5878
		TGGGAATA <u>ACATAAA</u> CT	5879
		AGTTTAT <u>GTT</u> ATTCCCA	5880
		TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCCTGTCA TTCTAGGTGGTGGT <u>AAAGGA</u> ACTCGTCTTCTCTTACAAGCA GAAGAGCTAAACCAGCTGTTCTATTGGTGG	5881
25	Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Val94Lys GTT-AAA	CCACCAATAGGAACAGCTGGTTAGCTCTGCTTGAAGAGGA AAAAGACGAGTT <u>CTT</u> ACCACCACTAGAATGACAGAGGCAACA GCTTTGGATCTGCCGTTGGTTCTCAA	5882
		TGGTGGT <u>AAAGGA</u> ACTC	5883

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GAGTCCTTACCA	5884
5 Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Pro122Leu CCA-CAA	CAAGCAGAAGAGCTAACCAAGCTTCCATTGGTGGTGTACCGGCTAATTGATGTACAAATGAGTAACTCGATTAACAGTGGCATACTGGAAAATTTCATCTAACACAGTTCAATT	5885
	GAATTGAACGTGTAAAGATGAAAATTTCGTATGCCACTGTTAA TGCAGTTACTCATTGTACATCAATTAGCCGGTAACAACCACCAATAGGAACAGCTGGTTAGCTCTGCTTG	5886
	TGATGTACAAATGAGTA	5887
	TACTCATTGTACATCA	5888
10 Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAT	CACAGTTCAATTCCCTTCCCTCAATCGTCACCTGCCGCACGTA TAATTTGAAATAACTGTGGTTGGAGATGGATTGTGGAGGTTT	5889
	TAGCTGCAACCCAGACTCCAGGGGATGC	
	GCATCCCTGGAGCTGGGTTGCAGCTAAACCTCCACAAATCCA TCTCCAAAACCCACATTATTCCAAAATTATACGTGCGGGCAAGGT	5890
	GACGATTGAGGGAAAAGGAATTGAAGTGT	
	TGGAAATAATGTGGTT	5891
15 Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAC	AACCCACATTATTCCA	5892
	CACAGTTCAATTCCCTTCCCTCAATCGTCACCTGCCGCACGTA TAATTTGAAATACGTGGTTGGAGATGGATTGTGGAGGTTT	5893
	AGCTGCAACCCAGACTCCAGGGGATGC	
	GCATCCCTGGAGCTGGGTTGCAGCTAAACCTCCACAAATCCA TCTCCAAAACCCACGTTATTCCAAAATTATACGTGCGGGCAAGGT	5894
	GACGATTGAGGGAAAAGGAATTGAAGTGT	
20 Increased Starch ADPGPP <i>Cicer arietinum</i> Ala101Lys GCT-AAA	TGGAAATAACGTGGTT	5895
	AACCCACGTTATTCCA	5896
	ACGTAGATTGGAAAAAGAGAGACCAAGTACAGTTGTAGCAATTAT	5897
	ACTAGGTGGAGGTAAAGGAACTCGTCCTCCCTCACCAAGCGACGAGCCAAGCCTGCTTCCAATTGGAGG	
	CCTCCAATTGGAACACAGCAGGCTTGGCTCGTCGCTGGTGAGAGGAAGAGACGAGTTCTTACCTCACCTAGTATAATTGCTACACTGTACTTGGGTCTCTTCCAAATCTACGT	5898
	TGGAGGTAAAGGAACCT	5899
	GAGTCCTTACCTCCA	5900

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased Starch ADPGPP <i>Cicer arietinum</i> Pro129Leu CCA-CTA	CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATA GGCTGATAGATGTACTAATGAGTAAC TGCACTCAATAGTGGGATCAA CAAAGTATACTACATTCTCACTCAATTAAATTCA	5901
		GAATTAAATTGAGTGAGAATGTACTTGTGATCCCACATTGAT GCAGTTACTCATTAGTACATCTATCAGCCTATAAGCACCTCCAATT GGAACAGCAGGCTTGGCTCGTCGCTTGG	5902
		AGATGTACTAATGAGTA	5903
		TACTCATTAGTACATCT	5904
		CTCAATTAAATTAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAATGTCACTTGGAGATGGCTATGTTGAGGTT CTTGCAGCAACTCAAACCTCCAGGGGAGCA	5905
10	Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAT	TGCTCCCTGGAGTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACATTAGTACCAAGAGTTAAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAAATTGAG	5906
		TGGTACTAATGTCACCT	5907
		AAGTGACATTAGTACCA	5908
		CTCAATTAAATTAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAACGTCACTTTGGAGATGGCTATGTTGAGGTT CTTGCAGCAACTCAAACCTCCAGGGGAGCA	5909
15	Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAC	TGCTCCCTGGAGTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACGTTAGTACCAAGAGTTAAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAAATTGAG	5910
		TGGTACTAACGTCACTT	5911
		AAGTGACGTTAGTACCA	5912
		ATATTGGAGAGGCCTCGGGCAAACCCCTAAGAATGTGGCTGCAATC ATACTGCCAGGCGGTAAAGGGACACACCTATTCCCTCTCACCAAT CGAGCTGCAACCCCTGCTGTTCCACTTGGAG	5913
20	Increased Starch ADPGPP <i>Ipomoea batatas</i> Ala94Lys GCA-AAA	CTCCAAGTGGAACAGCAGGGGTTGCAGCTCGATTGGTGAGAGGG AATAGGTGTGTCCTTTACCGCCTGGCAGTATGATTGAGCCACA TTCTTAGGGTTGCCGACGCCTCTCCAATAT	5914
		CAGGCCTTAAAGGGACA	5915
		TGTCCCTTACCGCCTG	5916
		CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGTGCTATA GGTTGATCGACATTCTAATGAGCAACTGCATCAACAGCGGGGTTA ACAAGATCTTGTGCTGACCCAGTTCAATT	5917
25	Increased Starch ADPGPP <i>Ipomoea batatas</i> Pro122Leu CCA-CTA	GAATTGAACGGGTCAAGCACAAAGATCTGTTAACCCGCTGTTG ATGCAGTTGCTCATTAGAATGTCGATCAACCTATAGCATCCTCAA GTGGAACAGCAGGGTTGCAGCTCGATTGG	5918
		CGACATTCTAATGAGCA	5919

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAT	TGCTCATTAGAATGTCG	5920
		TGACCCAGTTCAATTAGCTTCTTAACCGTCACATTCCCGTAC CGTCTTGGCAATA <u>ATGT</u> GAGCTTCGGAGATGGATTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5921
		GTTCCTTGTGTTGGTGCAGCCAGCACCTAACAAATCCA TCTCGAAGCTCACATTATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACGGTCA	5922
		TGGCAATA <u>ATGT</u> GAGCT	5923
		AGCTCACATTATTGCCA	5924
10	Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAC	TGACCCAGTTCAATTAGCTTCTTAACCGTCACATTCCCGTAC CGTCTTGGCAATA <u>ACGT</u> GAGCTTCGGAGATGGATTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5925
		GTTCCTTGTGTTGGTGCAGCCAGCACCTAACAAATCCA TCTCGAAGCTCACGTTATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACGGTCA	5926
		TGGCAATA <u>ACGT</u> GAGCT	5927
		AGCTCACGTTATTGCCA	5928
		CATTCCGGAGGAACCTTGCGGATCCAAATGAGGTTGCTGCTGTTA TATTGGGTGGTGGCAA <u>AGGG</u> ACTCAACTTTCTCTCACAGCA CAAGGGCCACGCCCTGCTGTTCTATTGGAGG	5929
15	Increased Starch ADPGPP <i>Oryza sativa</i> Thr96Lys ACC-AAA	CCTCCAATAGGAACAGCAGGCGTGGCCCTTGCTGCTGAGAGG AAAAAGTTGAGTCCC <u>TT</u> TGCCACCACCCAAATAACAGCAGCAAC CTCATTGATCCGCAAAGTTCTCCCGGAATG	5930
		TGGTGGCAA <u>AGGG</u> ACTC	5931
		GAGTCC <u>TT</u> TGCCACCA	5932
		CAAGCACAA <u>GGG</u> CCACGCCCTGCTGTTCTATTGGAGGATGCTATA GGCTTATCGATATCC <u>TC</u> CATGAGCACTGTTCAACAGTGGCATAAA CAAGATATTCTATA <u>ACT</u> CAATTCAACTC	5933
		GAGTTGAATTGAGTCATTATGAATATCTTGTTATGCCACTGTTGAA ACAGTTGCTCAT <u>GAGG</u> ATATCGATAAGCCTATAGCATCCTCCAATA GGAACAGCAGGCGTGGCCCTTGCTTG	5934
20	Increased Starch ADPGPP <i>Oryza sativa</i> Pro124Leu CCC-CTC	CGATATCC <u>TC</u> CATGAGCA	5935
		TGCTCAT <u>GAGG</u> ATATCG	5936
		TGACTCAATTCAACTCAGCATCTTAATCGTCACATTCACTGTCAC GTACCTGGTGG <u>AA</u> ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCGGAGGC	5937
		GCCTCCCCAGGGATTGTGAGCGGCTAACACCTAACAGAACCA TCAGTAAAGTTGATA <u>TT</u> ACCAACCAAGGTACGTACGATGAATGTGAC GATTAAGAGATGCTGAGTTGAATTGAGTC	5938

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGTGGTAATATCACT	5939
	AGTTGATATTACCACCA	5940
5 Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAC	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCACTCGTAC GTACCTTGGTGGTAACATCAACTTACTGATGGTTCTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	5941
	GCCTCCCCAGGCATTGTGAGCGGCTAACACCTAACAGAACCA TCAGTAAAGTTGATGTTACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA	5942
	TGGTGGTAACATCACT	5943
	AGTTGATGTTACCACCA	5944
10 Increased Starch ADPGPP <i>Triticum aestivum</i> Thr80Lys ACC-AAA	GTCCTTCAGGGAGGATAAGCGATCCGAACGAGGTTGCGGCCGTC ATACTCGGCGGCGGCAAAGGGACTCAGCTTCCCACTCACGAG CACAGGGCCACACCTGCTGTTCTATTGGAGG	5945
	CCTCCAATAGGAACACAGCAGGTGTGGCCCTTGTGCTCGTGAGTGG GAAGAGCTGAGTCCCCTTGCCGCCGCCAGTATGACGGCCGCAA CCTCGTTGGATCGCTTAATCCTCCTGAAGGAC	5946
	CGGCGGCCAAAGGGACTC	5947
	GAGTCCCCTTGCCGCCG	5948
15 Increased Starch ADPGPP <i>Triticum aestivum</i> Pro108Leu CCC-CTC	CGAGCACAAAGGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGACATTCTCATGAGCACTGCTCAACAGTGGCATCA ACAAGATATTGTCATGACCCAGTTCAACTC	5949
	GAGTTGAACGGGTCTGACGAATATCTGTTGATGCCACTGTTG AAGCAGTTGCTCATGAGAATGTCGATGAGCCTGTAACATCCTCCA ATAGGAACAGCAGGTGTGGCCCTTGTGCTCG	5950
	CGACATTCTCATGAGCA	5951
	TGCTCATGAGAATGTCG	5952
20 Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAT	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTACCGCA CCTACCTCGGCGGGAAATATCAATTCACTGATGGATCCGTTGAGG TATTGGCCCGGACGCAAATGCCGGGGAGGC	5953
	GCCTCCCCGGCATTGCGTCGCGGCCAACACCTAACGGATCC ATCAGTGAATTGATATTCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGTCA	5954
	CGGCGGGAAATATCAATT	5955
	AATTGATATTCCGCCG	5956
25 Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAC	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTACCGCA CCTACCTCGGCGGGAAACATCAATTCACTGATGGATCCGTTGAGG TATTGGCCCGGACGCAAATGCCGGGGAGGC	5957

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.	
	GCCTCCCCGGGCATTGCGTCGCGGCCAATACCTAACGGATCC ATCAGTGAAATTGAT <u>GTT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACGGTCA	5958	
	CGGCGGG <u>AAC</u> ATCAATT	5959	
	AATTGAT <u>GTT</u> CCCGCCG	5960	
5	Increased Starch ADPGPP <i>Oryza sativa</i> Thr95Lys ACT-AAA	CCTCCCAGAAAGATTATGCTGATGCAAGGCCACGTTCTGCTGTCA TTTGGGGTGGAGGCA <u>AAGGAG</u> TTCAACTCTTCCTGTGACAAGCA CAAGGGCTACCCCCGCTGTTCTGTGGAGG	5961
		CCTCCAACAGGAACAGCGGGGGTAGCCCTTGTGCTTGTCAAGGG AAAGAGTTGAAC <u>CC</u> <u>TT</u> GCCTCCACCCAAAATGACAGCAGAAC GTGGCTTGATCAGCATAATTCTTCGGGAGG	5962
		TGGAGG <u>CAAAGGAG</u> TTC	5963
		GAAC <u>ACTCC</u> <u>TT</u> GCCTCCA	5964
	Increased Starch ADPGPP <i>Oryza sativa</i> Pro123Leu CCT-CTT	CAAGCACAAGGGCTACCCCCGCTGTTCTGTGGAGGATGTTACA GGCTTATTGACAT <u>CC</u> <u>TT</u> ATGAGCAATTGCTTCAATAGCGGAATAAA TAAAATATTGTGATGACTCAG <u>TT</u> CAATT	5965
10		GAATTGAAC <u>TGAGT</u> CATCACAAATATT <u>TT</u> ATTCCGCTATTGAA GCAATTGCTCATA <u>AGGAT</u> GTCAATAAGCCTGTAACATCCTCCAACA GGAACAGCGGGGGTAGCCCTTGTGCTTG	5966
		TGACAT <u>CC</u> <u>TT</u> ATGAGCA	5967
		TGCTCATA <u>AGGAT</u> GTCA	5968
	Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAT	TGACTCAG <u>TT</u> CAATTCTGCTTCTTAATGCCATATCCATCATA ATAC <u>CTTGGTGGGAA</u> AT <u>CAAC</u> TTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5969
		GGTCGT <u>CAGG</u> CATTGTGAGCAG <u>CC</u> AATACCTGCACAGACCCA TCAGTAAAG <u>TTGAT</u> <u>TT</u> CCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAA <u>TTGAA</u> CTGAGTCA	5970
15		TGGTGG <u>GAAT</u> AT <u>CAACT</u>	5971
		AGTTGAT <u>TT</u> CCCACCA	5972
	Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAC	TGACTCAG <u>TT</u> CAATTCTGCTTCTTAATGCCATATCCATCATA ATAC <u>CTTGGTGGGAA</u> AC <u>ATCAAC</u> TTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5973
		GGTCGT <u>CAGG</u> CATTGTGAGCAG <u>CC</u> AATACCTGCACAGACCCA TCAGTAAAG <u>TTGAT</u> <u>TT</u> CCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAA <u>TTGAA</u> CTGAGTCA	5974
		TGGTGG <u>GAAC</u> AT <u>CAACT</u>	5975
20		AGTTGAT <u>GT</u> CCCACCA	5976

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased Starch ADPGPP <i>Triticum aestivum</i> Thr99Lys ACC-AAA	CCTTCGGCAGGAATTACGCCGATCCGAACGAGGTCGCCGCGTC ATACTCGGCGGTGGCA <u>AAGG</u> GACTCAGCTCTCCCTCTCACAAG CACAAGGCCACACCTGCTGTTCTATTGGAGG	5977
	CCTCCAATAGGAACACAGCAGGTGTGGCCCTGTGCTTGAGAGG GAAGAGCTGAGTCCC <u>TT</u> GCCACCGCCGAGTATGACGGCCGCA CCTCGTTCGGATCGCGTAATTCCCTGCGGAAGG	5978
	CGGTGGCA <u>AAGG</u> ACTC GAGTCCC <u>TT</u> GCCACCG	5979 5980
	CAAGCACAAGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGATATT <u>C</u> CATGAGCACTGCTCAATAGTGGCATCAA CAAGATATT <u>C</u> GTATGACGCA <u>GT</u> CAACTC GAGTTGA <u>CT</u> CGTCATGACGA <u>AT</u> ATCTGTTGATGCCACTATTGA AGCAGTTGCTCAT <u>G</u> AGA <u>AT</u> ATCGATGAGCCTGTAACATCCTCAA TAGGAACACAGCAGGTGTGGCCCTGTGCTTG CGATATT <u>C</u> CATGAGCA TGCTCAT <u>G</u> AGA <u>AT</u> ATCG	5981 5982 5983 5984
10 Increased Starch ADPGPP <i>Triticum aestivum</i> Pro127Leu CCC-CTC	TGACGCAGTCAACTCGGCCTCTCTTAATCGTCACATTACCGCA CCTACCTCGGCGGG <u>A</u> ATCAATT <u>C</u> ACTGATGGATCTGTTGAGG TATTGGCCCGACGCAA <u>AT</u> GCCCGGGAGGC	5985
	GCCTCCCCGGGCATT <u>T</u> CGTCGCGGCCA <u>AT</u> ACCTCAACAGATCC ATCAGTGA <u>AT</u> TGAT <u>AT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGGCGAGTTGA <u>CT</u> CGTCA	5986
	CGGC <u>GGG</u> <u>A</u> AT <u>T</u> CAATT AATTGAT <u>AT</u> CCCGCCG	5987 5988
	TGACGCAGTCAACTCGGCCTCTCTTAATCGTCACATTACCGCA CCTACCTCGGCGGG <u>A</u> AT <u>C</u> AA <u>TT</u> CA <u>CT</u> GATGGATCTGTTGAGG TATTGGCCCGACGCAA <u>AT</u> GCCCGGGAGGC GCCTCCCCGGGCATT <u>T</u> CGTCGCGGCCA <u>AT</u> ACCTCAACAGATCC ATCAGTGA <u>AT</u> TGAT <u>GT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGGCGAGTTGA <u>ACT</u> CGTCA CGGC <u>GGG</u> <u>A</u> AT <u>C</u> AATT AATTGAT <u>GT</u> CCCGCCG	5989 5990 5991 5992
25 Increased Starch ADPGPP <i>Zea mays</i> Thr96Lys ACC-AAA	CTTTCGGAGGAATTATGCTGATCTAATGAAGTCGCTGCCGTCA TTTG <u>GGG</u> GTGGTGG <u>A</u> <u>AGG</u> GACTCAGCT <u>TT</u> CCCTCTCACAAGCA CAAGGGCCACCCCTGCTGTTCTATTGGAGG	5993
	CCTCCAATAGGAACACAGCAGGGTGGCCCTGTGCTTGAGAGG GAAAAGCTGAGTCCC <u>TT</u> ACCACCA <u>CC</u> AA <u>AT</u> GACGGCAGCGAC TTCATTAGGATCAGCATAATTCCCTCGAAAAG TGGTGG <u>A</u> <u>AGG</u> ACTC	5994 5995

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTCCCTTACCA	5996
5 Increased Starch ADPGPP <i>Zea mays</i> Pro124Leu CCC-CTC	CAAGCACAAGGGCCACCCCTGCTGTCCTATTGGAGGATGTTACA GGCTTATTGATATCC <del>T</del> CATGAGCAACTGTTCAACAGTGGCATAAA CAAGATATTGTTATGACTCAGTTCAACTC	5997
	GAGTTGAAC TGAGTCATAACAAATATCTTGTATGCCACTGTTGA AACAGTTGCTCATGAGGATATCAATAAGCCTGTAACATCCTCCAAT AGGAACAGCAGGGTGGCCCTGTGCTT	5998
	TGATATCC <del>T</del> CATGAGCA	5999
	TGCTCATGAGGATATCA	6000
10 Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAT	TGACTCAGTTCAACTCAGCTCTTAACCGTCACATTCACTCGTAC CTATCTTGGTGGGA <del>A</del> ATCAACTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCCTGGGGAGGC	6001
	GCCTCCCCAGGCATTGTGTTGCAGCCAGCACCTAACAGATCCA TCAGTGAAGTTGATATTCCCACCAAGATAAGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAAC TGAGTC	6002
	TGGTGGGA <del>A</del> ATATCAACT	6003
	AGTTGATATTCCCACCA	6004
15 Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAC	TGACTCAGTTCAACTCAGCTCTTAACCGTCACATTCACTCGTAC CTATCTTGGTGGGA <del>A</del> ACATCAACTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCCTGGGGAGGC	6005
	GCCTCCCCAGGCATTGTGTTGCAGCCAGCACCTAACAGATCCA TCAGTGAAGTTGATGTTCCCACCAAGATAAGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAAC TGAGTC	6006
	TGGTGGGA <del>A</del> ACATCAACT	6007
	AGTTGATGTTCCCACCA	6008
20 Increased Starch ADPGPP <i>Solanum tuberosum</i> Ala58Lys GCG-AAG	CTTGAGAGGCAAAAGAAGGGCGATGCAAGGACAGTAGTAGCAAT CATTCTAGGAGGGGGAA <del>AG</del> GGAACTCGTCTTCCCCCTACCAA ACGTCGTGCTAACGCTGCCGTTCCAATGGGAG	6009
	CTCCCATTGGAACGGCAGGCTTAGCACGACGTTGGTGGGG AAAAGACGAGTTCCC <del>T</del> CCCCCTCCTAGAATGATTGCTACTACTG TCCTTGATGCCCTCTTTGCCCTCAAG	6010
	GAGGGGGAA <del>AG</del> GGAACT	6011
	AGTTCCCTTCCCCCTC	6012
25 Increased Starch ADPGPP <i>Solanum tuberosum</i> Pro86Leu CCA-CTA	CCAAACGTCGTGCTAACGCTGCCGTTCCAATGGGAGGAGCATATA GGCTAATTGATGTAC <del>A</del> ATGAGCAACTGTTAACAGTGGCATAA CAAAGTATAACATTCTCACTCAATTCAACTC	6013
	GAGTTGAATTGAGTGAGAATGTATACTTTGATGCCACTGTTAA TACAGTTGCTCATTAGTACATCAATTAGCCTATATGCTCCTCCCAT TGGAACGGCAGGCTTAGCACGACGTTGG	6014

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATGTACTAATGAGCA	6015
	TGCTCATTAGTACATCA	6016
5 Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAT	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTGGCAAT <u>AAT</u> GTACATTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6017
	AATTACACCTGGTGTGAGTTGCTGCTAACAGACCTCGACATAGCCA CTCTCGAATGTGAC <u>ATT</u> ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGAAGGCTGAGTTGAATTGAG	6018
	TGGCAAT <u>AAT</u> GTACAT	6019
	ATGTGAC <u>ATT</u> ATTGCCA	6020
	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTGGCAAT <u>AC</u> GTACATTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6021
10 Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAC	AATTACACCTGGTGTGAGTTGCTGCTAACAGACCTCGACATAGCCA CTCTCGAATGTGAC <u>G</u> <u>TT</u> ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGAAGGCTGAGTTGAATTGAG	6022
	TGGCAAT <u>AC</u> GTACAT	6023
	ATGTGAC <u>G</u> <u>TT</u> ATTGCCA	6024
	TATTTGAATCTCCAAAAGCTGACCCAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGTAA <u>AGGG</u> ACTCGCCTTTCCCTTACTAGCA GGAGAGCTAACGCCAGCAGTGCCAATTGGAGG	6025
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCCAGT <u>CCC</u> <u>TT</u> ACCAACCACCCAGCACAATTGCAGCCACA <u>TTTTTGGGT</u> CAG <u>TTTGG</u> GAGATTCAAATA	6026
15 Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAA	TGGTGGTAA <u>AGGG</u> ACTC	6027
	GAGT <u>CCC</u> <u>TT</u> ACCAACCA	6028
	TATTTGAATCTCCAAAAGCTGACCCAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGTAA <u>AC</u> <u>GGG</u> ACTCGCCTTTCCCTTACTAGCA GGAGAGCTAACGCCAGCAGTGCCAATTGGAGG	6029
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCCAGT <u>CCC</u> <u>TT</u> ACCAACCACCCAGCACAATTGCAGCCAC <u>ATTTTGGGT</u> CAG <u>TTTGG</u> GAGATTCAAATA	6030
	TGGTGGTAA <u>AC</u> <u>GGG</u> ACTC	6031
20 Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAC	GAGT <u>CCC</u> <u>TT</u> ACCAACCA	6032
	CTAGCAGGAGAGCTAACGCCAGCAGTGCCAATTGGAGGGTGTAC AGGCTGATTGATGTGCT <u>TT</u> ATGAGCAACTGCATCAACAGTGGCATT	6033
	AGAAAGATTTCATTCTACCCAGTTCAATT	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GAATTGAAC TGGGTAAAGAATGAAAATCTTCTAATGCCACTGTTGA TGCAGTTGCTCAT <u>A</u> GCACATCAATCAGCCTGTAACACCCCTCAA TTGGCACTGCTGGCTTAGCTCTCCTGCTAG	6034
	TGATGTGCT <u>T</u> ATGAGCA	6035
	TGCTCAT <u>A</u> GCACATCA	6036
5 Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAT	CCCAGTTCAATT <u>C</u> GTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTGGAGATA <u>A</u> ATGTGAATTGGGGATGGCTTGTGGAGGTT TTTGCTGCTACACAAACACCTGGAGAATC	6037
	GATTCTCCAGGTGTTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATT <u>C</u> AC <u>T</u> ATCTCCAAAATTATAGGTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	6038
	TGGAGATA <u>A</u> ATGTGAATT	6039
	AATT <u>C</u> AC <u>T</u> ATCTCCA	6040
	CCCAGTTCAATT <u>C</u> GTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTGGAGATA <u>A</u> ACGTGAATTGGGGATGGCTTGTGGAGGTT TTTGCTGCTACACAAACACCTGGAGAATC	6041
10 Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAC	GATTCTCCAGGTGTTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATT <u>C</u> AC <u>G</u> TTATCTCCAAAATTATAGGTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	6042
	TGGAGATA <u>A</u> ACGTGAATT	6043
	AATT <u>C</u> AC <u>G</u> TTATCTCCA	6044

**Table 21**  
**Oligonucleotides to produce plants with waxy starch**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser12Term TCA-TGA	GAATCCAGGTAAACGGGTAGTCATAATGGCAACTGTGACTGCTTC TTCTAACTTGTGT <u>GAAGAAC</u> TTCACTTTCAACAATCATGGTGCTT CTTCATGCTCTGATGTCGCTCAGATTAC	6045
		GTAATCTGAGCGACATCAGAGCATGAAGAACCCATGATTGTTGA AAAGTGAAGTTCTT <u>CACACAAAG</u> TTAGAAGAACAGTCACAGTTGC CATTATGAAC <del>T</del> ACCCGTTACCTGGATT	6046
		CTTTGTGT <u>GAAGAAC</u> TT	6047
		AAGTTCTT <u>CACACAAAG</u>	6048
10	Waxy starch GBSS <i>Arabidopsis thaliana</i> Arg13Term AGA-TGA	ATCCAGGTAAACGGGTAGTCATAATGGCAACTGTGACTGCTTCTT CTAACTTGTGT <u>CA</u> TA <u>GAAC</u> TTCACTTTCAACAATCATGGTGCTTCT TCATGCTCTGATGTCGCTCAGATTACCT	6049
		AGGTAATCTGAGCGACATCAGAGCATGAAGAACCCATGATTGTT GAAAAGTGAAG <u>TTCA</u> GACACAAAGTTAGAAGAACAGTCACAGTT GCCATTATGAAC <del>T</del> ACCCGTTACCTGGAT	6050
		TTGTGT <u>CA</u> TA <u>GAAC</u> TTCA	6051
		TGAAG <u>TTCA</u> GACACAA	6052
		TAAACGGGTAGTCATAATGGCAACTGTGACTGCTTCTTCAACTT TGTGT <u>CAAGAAC</u> TT <u>GACT</u> TTCAACAATCATGGTGCTTCTTCATGCT CTGATGTCGCTCAGATTACCTTAAAGG	6053
15	Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA	CCTTTAAGGTAA <u>CTGAGCGACATCAGAGCATGAAGAACCCAT</u> GATTGTTGAA <u>AGTCAAGTTCTGACACAAAGTTAGAAGAACAGT</u> CACAGTTGCCATTATGAAC <del>T</del> ACCCGTTA	6054
		AAGAAC <u>TTGACT</u> TTCA	6055
		TGAAAAGT <u>CAAGTTCTT</u>	6056
		TGACTGCTCTTCAACTTTGTGT <u>CAAGAAC</u> TTCAACAAAT CATGGTGCTTCTT <u>GATGCTCTGATGTCGCTCAGATTACCTTAAAG</u> GCCAA <u>TCCTTGACTCATTGTGGGTTAAG</u>	6057
20	Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser24Term TCA-TGA	CTTAACCCACAATGAGTCAGGATTGGCCTTAA <u>GGTAATCTGAG</u> CGACATCAGAGCAT <u>CAAGAACCCATGATTGTTGAAAGTGAAGT</u> TCTTGACACAAAGTTAGAAGAACAGTC	6058
		TGCTTCTT <u>GATGCTCTG</u>	6059
		CAGAGCAT <u>CAAGAAC</u> CA	6060

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Arabidopsis thaliana</i> Cys25Term TGC-TGA	TGCTTCTTCTAACCTTGTCAGAACCTCACTTTCAACAATCATG GTGCTTCTCATGATCTGATGTCGCTCAGATTACCTTAAAGGCCA ATCCTTGACTCATTGGGTTAAGGTCA	6061
		TGACCTAACCCACAATGAGTCAGGATTGGCCTTTAAGGTAATC TGAGCGACATCAGATCATGAAGAAGCACCATTGATTGTTGAAAAGTG AAGTTCTTGACACAAAGTTAGAAGAAGCA	6062
		TCTTCATGATCTGATGT	6063
		ACATCAGATCATGAAGA	6064
10	Waxy starch GBSS <i>Antirrhinum majus</i> Lys24Term AAA-TAA	GTAACAGCTTCACAGTGGTGTACATGTCCATGGTGGAGCAACG TCTTCACCGGATACTAAACAAACTTGGCCAGGTTGGCCTCAGG AACCAGCAATTCACTACAATGGGTTGAGAT	6065
		ATCTCAACCCATTGTGAGTGAATTGCTGGTCCCTGAGGCCAACCT GGGCCAAGTTGTTAAAGTATCCGGTGAAGACGTTGCTCCACCAT GGACATGTGACACCAACTGTGAAGCTGTTAC	6066
		CGGATACTAAACAAAC	6067
		GTGGTTAAAGTATCCG	6068
15	Waxy starch GBSS <i>Antirrhinum majus</i> Leu27Term TTG-TAG	CACAGTTGGTGTACATGTCCATGGTGGAGCAACGTCTTCACCGG ATACTAAAACAAACTAGGCCAGGTTGGCCTCAGGAACCAGCAAT TCACTCACAATGGGTTGAGATCAATAAACAT	6069
		ATGTTTATTGATCTAACCCATTGTGAGTGAATTGCTGGTCCCTGA GGCCAACCTGGGCTAGTTGTTAGTATCCGGTGAAGACGTTG CTCCACCATGGACATGTGACACCAACTGTG	6070
		AACAAACTAGGCCAGG	6071
		CCTGGGCCAGTTGTT	6072
20	Waxy starch GBSS <i>Antirrhinum majus</i> Gln29Term CAG-TAG	TTGGTGTACATGTCCATGGTGGAGCAACGTCTTCACCGGATACT AAAACAAACTGGCCTAGGTTGGCCTCAGGAACCAGCAATTCACT CACAATGGGTTGAGATCAATAAACATGGTG	6073
		CAACCATGTTATTGATCTAACCCATTGTGAGTGAATTGCTGGTT CCTGAGGCCAACCTAGGCCAAGTTGTTAGTATCCGGTGAAGA CGTTGCTCCACCATGGACATGTGACACCAA	6074
		ACTTGGCCAGTTGGC	6075
		GCCAACCTAGGCCAAGT	6076
25	Waxy starch GBSS <i>Antirrhinum majus</i> Gln35Term CAG-TAG	GGTGGAGCAACGTCTTCACCGGATACTAAAACAAACTGGCCCAG GTTGGCCTCAGGAACCTAGCAATTCACTCACAATGGGTTGAGATCAA TAAACATGGTTGATAAGCTTCAAATGAGGA	6077
		TCCTCATTGAAAGCTTATCAACCATGTTATTGATCTAACCCATTG TGAGTGAATTGCTAGTTCCCTGAGGCCAACCTGGCCAAGTTGTT TTAGTATCCGGTGAAGACGTTGCTCCACC	6078

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCAGGAAC <u>T</u> AGCAATT	6079
	GAATTG <u>C</u> TAGTTCTGA	6080
5 Waxy starch GBSS <i>Antirrhinum majus</i> Gln36Term CAA-TAA	GGAGCAACGTCTCACCGGATACTAAAACAAACTGGCCCAGGTT GGCCTCAGGAACCAG <u>T</u> AATTCACTCACAAATGGGTTGAGATCAATAA ACATGGTTGATAAGCTCAAATGAGGAACA	6081
	TGTTCTCATTTGAAGCTTATCAACC <u>T</u> ATGTTATTGATCTCAACCCA TTGTGAGTGAATT <u>A</u> CTGGTCTGAGGCCAAC <u>T</u> GGGCCAAGTT	6082
	GTTTAGTATCCGGTGAAGACGTTGCTCC GGAACC <u>A</u> GTAA <u>T</u> CACT	6083
	AGTGAATT <u>A</u> CTGGTTCC	6084
10 Waxy starch GBSS <i>Ipomoea batatas</i> Gly20Term GGA-TGA	GTGATGGCGACTATAACTGCCTCACACTTGTTCATGTCTGTG GGGGTGCCACTTCT <u>T</u> GAGAATCAAAGTGGGTTGGGTCATTAG CCCTGAGGAGCCAAG <u>C</u> GTGTGACTCACATG	6085
	CATTGTGAGTCACAGCTGGCTCCTCAGGGCTAATTGACCCACC CCACTTTGATT <u>CTC</u> <u>A</u> AGAAGTGGCACCCCCACAGACATGAGAAA CAAAGTGTGAGGCAGTTATAGTCGCCATCAC	6086
	CCACTTCT <u>T</u> GAGAATCA	6087
	TGATTCT <u>C</u> <u>A</u> AGAAGTGG	6088
15 Waxy starch GBSS <i>Ipomoea batatas</i> Glu21Term GAA-TAA	ATGGCGACTATAACTGCCTCACACTTGTTCATGTCTGTGGGG GTGCCACTCTGG <u>A</u> ATCAAAGTGGGTTGGGTCATTAGCCC TGAGGAGCCAAG <u>C</u> GTGTGACTCACATGGGT	6089
	ACCCATTGTGAGTCACAGCTGGCTCCTCAGGGCTAATTGACCC ACCCCCACTTTGATT <u>ATCC</u> CAGAAGTGGCACCCCCACAGACATGAG AAACAAAGTGTGAGGCAGTTATAGTCGCCAT	6090
	CTTCTGG <u>A</u> ATCAAA	6091
	TTTGATT <u>ATCC</u> CAGAAG	6092
20 Waxy starch GBSS <i>Ipomoea batatas</i> Ser22Term TCA-TGA	CGACTATAACTGCCTCACACTTGTTCATGTCTGTGGGGTGC CACTTCTGG <u>A</u> ATGAAAGTGGGTTGGGTCATTAGCCCTGAG GAGCCAAG <u>C</u> GTGTGACTCACATGGGTTGAG	6093
	CTCAACCCATTGTGAGTCACAGCTGGCTCCTCAGGGCTAATTGA CCCAACCCCCACTTT <u>C</u> ATTCTCCAGAAGTGGCACCCCCACAGACA TGAGAAACAAAGTGTGAGGCAGTTATAGTCG	6094
	TGGAGAAT <u>G</u> AAAAGTGG	6095
	CCACTTT <u>C</u> ATTCTCCA	6096

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Ipomoea batatas</i> Lys23Term AAA-TAA	ACTATAACTGCCTCACACTTGTTCATGTCGTGGGGTGCCTA CTTCTGGAGAATCAT <u>A</u> AGTGGGGTGGTCAATTAGCCCTGAGGA GCCAAGCTGTGACTCACAA <u>T</u> GGGCTCAGGGCTAATT	6097
		GACCAACCCCCACTT <u>A</u> TGATTCTCCAGAA <u>G</u> GTGGCACCCCCACAGA	6098
		CATGAGAA <u>A</u> AAAGTGTGAGGCAGTTAGT	
		GAGAA <u>T</u> AGTGGGG	6099
		CCCCACTT <u>A</u> TGATTCTC	6100
10	Waxy starch GBSS <i>Ipomoea batatas</i> Leu26Term TTG-TAG	CCTCACACTTGTTCATGTCGTGGGGTGCCTA <u>T</u> CTGGAGA ATCAAAAGTGGGGT <u>A</u> GGGTCAATTAGCCCTGAGGAGCCAGCTGT	6101
		GA <u>T</u> TCACA <u>A</u> GGGTGAGACCTGTGAACAA	
		TTGTTCACAGGTCTCAACCCATTGTGAGTCACAGCTGGCTCCTCA GGGCTAATTGACCC <u>T</u> ACCCCCACTT <u>T</u> GATTCTCCAGAA <u>G</u> GTGGCAC	6102
		CCCCACAGACATGAGAA <u>A</u> AAAGTGTGAGG	
		AGTGGGGT <u>A</u> GGGTCAAT	6103
15	Waxy starch GBSS <i>Astragalus membranaeus</i> Tyr8Term TAT-TAG	ATCGGCGATTGGCTCCTACTGCTCTCACAGAA <u>T</u> GGCAC GGTGACGGGGCTT <u>A</u> GGTGGTGT <u>C</u> GAGAA <u>G</u> CGCGTGCTCAATT <u>C</u>	6105
		CCAGGGAA <u>A</u> ACAGAA <u>G</u> CCAA <u>G</u> TGAATT <u>C</u> A	
		TGAATT <u>C</u> ACTTGGCTCTGTT <u>C</u> CC <u>T</u> GGGAATT <u>G</u> AGCAGCG CTTCTGACACC <u>C</u> TAAGACCCCGTCACC <u>T</u> GGCCATT <u>T</u> GTGA	6106
		GAGAGCAGTAAGGAGCAAC <u>A</u> TCGCCGAT <u>G</u>	
		GGGTCTT <u>A</u> GGTGGTG <u>C</u>	6107
20	Waxy starch GBSS <i>Astragalus membranaeus</i> Ser11Term TCG-TAG	GACACCAC <u>C</u> TAAGACCC	6108
		ATTGTTGCTCCTACTGCTCTCACAGAA <u>T</u> GGCAACGGTGACGG GGTCTT <u>A</u> GGTGT <u>G</u> AGAGAA <u>G</u> CGCGTGCTCAATT <u>C</u> CCAGGGAA	6109
		GAACAGAA <u>G</u> CCAA <u>G</u> TGAATT <u>C</u> ACCTCAGAA	
		TTCTGAGGTGAATT <u>C</u> ACTTGGCTCTGTT <u>C</u> CC <u>T</u> GGGAATT <u>G</u> AGCAC <u>G</u> CGCT <u>T</u> CT <u>C</u> ACACCACATAAGACCCCGTCACC <u>T</u> GGCC	6110
		TTCTGTGAGAGAGCAGTAAGGAGCAACAA <u>T</u>	
		TGTGGTGT <u>A</u> AGAGAA <u>G</u> CG	6111
		CGCTTCT <u>C</u> ACACCACAA	6112

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Astragalus membranaeus</i> Arg12Term AGA-TGA	TGTTGCTCCTACTGCTCTCACAGAATGGCAACGGTGACGGGG TCTTATGTTGGTGTGCGTGAAGCGCGTGCCTCAATTCCCAGGGAAAGA ACAGAAGCCAAAGTGAATTCACCTCAGAAGA	6113
	TCTTCTGAGGTGAATTCACTTGGCTTGTCTCCCTGGGAATT GAAGCACGCGCTTCACGACACCACATAAGACCCCGTACCGTTGC CATTCTGTGAGAGAGCAGTAAGGAGCAACA	6114
	TGGTGTGCGTGAAGCGCG	6115
	CGCGCTTCACGACACCA	6116
10 Waxy starch GBSS <i>Astragalus membranaeus</i> Cys15Term TGC-TGA	ACTGCTCTCACAGAATGGCAACGGTGACGGGGCTTATGGT GTCGAGAACGCGGTGATTCAATTCCCAGGGAAAGAACAGAACCAA AGTGAATTCACCTCAGAAGATAATCTCAAT	6117
	ATTGAGATTATCTCTGAGGTGAATTCACTTGGCTTGTCTTC CCTGGGAATTGAATCACGCGCTCTCGACACCACATAAGACCCCG TCACCGTTGCCATTCTGTGAGAGAGCAGT	6118
	AGCGCGTGATTCAATTCA	6119
	GAATTGAATCACGCGCT	6120
15 Waxy starch GBSS <i>Astragalus membranaeus</i> Gln19Term CAG-TAG	CACAGAATGGCAACGGTGACGGGGCTTATGGTGTGAGAACG GCGTCTCAATTCTAGGGAAAGAACAGAACCAAAGTGAATTCA CCTCAGAAGATAAACTCAATAGCCAAGCAT	6121
	ATGCTTGGCTATTGAGATTATCTCTGAGGTGAATTCACTTGGCT TCTGTTCTCCCTAGGAATTGAAGCACGCGCTCTCGACACCACAT AAGACCCCGTCACCGTTGCCATTCTGTG	6122
	TCAATTCTAGGGAAAGA	6123
	TCTTCCCTAGGAATTGA	6124
20 Waxy starch GBSS <i>Solanum tuberosum</i> Ser7Term TCA-TGA	TGTAGCTTGGTAGATTCCCCTTTGTAGACCACACATCACATGGC AAGCATCACAGCTTGACACCACCTTGTGCAAGAACCAAACCTCA CTAGACACCAATCAACCTTGTACAGAT	6125
	ATCTGTGACAAGGTTGATTGGTGTCTAGTAAGTTGGCTTGT ACACAAAGGGTGTCAAGCTGTGATGCCATGTGATGTG TCTACAAAAGGGAAATCTACCAAGCTACA	6126
	CACAGCTTGACACCACT	6127
	AGTGGTGTCAAGCTGTG	6128
25 Waxy starch GBSS <i>Solanum tuberosum</i> Ser12Term TCA-TGA	TCCCCTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTC ACACCACTTGTGAAAGAACCAAACCTCACTAGACACCAAAATCA ACCTTGTACAGATAGGACTCAGGAACCA	6129
	TGGTTCCCTGAGTCCTATCTGTGACAAGGTTGATTGGTGTAGTG AAGTTGGCTTCTCACACAAAGTGGTGTGAAGCTGTGATGCTTGC CATGTGATGTGGTCTACAAAAGGGGA	6130

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTTTGTGT <u>GAAGAAGCC</u>	6131
	GGCTTCTT <u>CACACAAAG</u>	6132
5 Waxy starch GBSS <i>Solanum tuberosum</i> Arg13Term AGA-TGA	CCCTTTTGAGACCACACATCACATGGCAAGCATCACAGCTTCAC ACCACTTTGTGT <u>CATGAAGCCAAACTC</u> ACTAGACACCAATCAAC CTTGTCA <u>CACAGATAGGACTCAGGAACCATA</u>	6133
	TATGGTTCTGAGTCCTATCTGTGACAAGGTTGATTGGTGTCTAG TGAAGTTGGCTT <u>CATGACACAAAGTGGTGTGAAGCTGTGATGCTT</u> GCCATGT <u>GATGTGGTCTACAAAAAGGG</u>	6134
	TTGTGT <u>CATGAAGCCAA</u>	6135
	TTGGCTT <u>CATGACACAA</u>	6136
	TTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACT TTGTGT <u>CAAGAACGCTAAACTTC</u> ACTAGACACCAATCAACCTTGT ACAGATAGGACTCAGGAACCATACTCTGA	6137
10 Waxy starch GBSS <i>Solanum tuberosum</i> Gln15Term CAA-TAA	TCAGAGTATGGTTCTGAGTCCTATCTGTGACAAGGTTGATTGGT GTCTAGTGAAGTT <u>AGCTTCTTGACACAAAGTGGTGTGAAGCTGTG</u> ATGCTGCCATGTGATGTGGTCTACAA	6138
	CAAGAACG <u>CTAAACTCA</u>	6139
	TGAAGTT <u>AGCTTCTTG</u>	6140
	CCACACATCACATGGCAAGCATCACAGCTTCACACCA <u>CTTGTGTC</u> AAGAACG <u>CCAAACTTGACT</u> AGACACCAATCAACCTTGT <u>CACAGATA</u> G <u>GACTCAGGAACCATACTCTGACTCACAA</u>	6141
	TTGTGAGTCAGAGTATGGTTCTGAGTCCTATCTGTGACAAGGTTG ATTTGGTGT <u>CTAGTCAGTTGGCTTCTTGACACAAAGTGGTGTGA</u> AGCTGTGATGCTGCCATGTGATGTGG	6142
15 Waxy starch GBSS <i>Solanum tuberosum</i> Ser17Term TCA-TGA	CCAA <u>ACTTGACTAGACA</u>	6143
	TGTCTAGT <u>CAAGTTGG</u>	6144
	GTCGATCACTCTCTCACCGCCGAAACAGATTTGACACAAAAA TGGCAACATAACGT <u>GATCTTCAATGCCGACGAGAACCGCGTGCT</u> TCAATTACCAAGGAAGATCAGCAGAGTCTA	6145
	TAGACTCTGCTGATCTTCTTGGTAATTGAGCACGCCGGTCTCGT CGGCATTGAAGAT <u>CACGTTATTGTTGCCATTGGTGTCAAATCT</u> GTTTCGGCGGTGAGAGAACAGAGTGTGAC	6146
	CAATAACGT <u>GATCTTCA</u>	6147
20 Waxy starch GBSS <i>Pisum sativum</i> Gly6Term GGA-TGA	TGAAGAT <u>CACGTTATTG</u>	6148

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Pisum sativum</i> Ser8Term TCA-TGA	ACTCTTCTCTCACCGCCGAAACAGATTTGACACAAAAATGGCAAC ATAACGGGATCTT <u>G</u> AATGCCGACGAGAACCGCGTGCTCAATT CCAAGGAAGATCAGCAGAGTCTAAACTGAA	6149
		TTCACTGAGACTCTGCTGATCTCCTTGGTAATTGAAGCACGCGG TTCTCGTGGCATT <u>C</u> AAGATCCCCTATTGTTGCCATTGGTGC AAAATCTGTTCGGCGGTGAGAGAAGAGT	6150
		GGGATCTT <u>G</u> AATGCCGA	6151
		TCGGCATT <u>C</u> AAGATCCC	6152
10	Waxy starch GBSS <i>Pisum sativum</i> Arg12Term AGA-TGA	ACCGCCGAAACAGATTTGACACAAAAATGGCAACAATAACGGGAT CTTCAATGCCGACGT <u>G</u> AACCGCGTGCTCAATTACCAAGGAAGAT CAGCAGAGTCTAAACTGAATT <u>G</u> CCTCAGA	6153
		TCTGAGGCAAATT <u>C</u> AGTTAGACTCTGCTGATCTCCTTGGTAATT GAAGCACCGCGGTT <u>C</u> ACGTGGCATTGAAGATCCCCTATTGTTGC CATTTTGTTGTCAAAATCTGTTGGCGGT	6154
		TGCCGACGT <u>G</u> AACCGCG	6155
		CGCGGTT <u>C</u> ACGTGGCA	6156
		AGATTTGACACAAAAATGGCAACAATAACGGGATCTCAATGCCG ACGAGAACCGCGTG <u>A</u> TTCAATTACCAAGGAAGATCAGCAGAGTCT AAACTGAATT <u>G</u> CCTCAGATACTTCAT	6157
15	Waxy starch GBSS <i>Pisum sativum</i> Cys15Term TGC-TGA	ATTGAAGTGTATCTGAGGCAAATT <u>C</u> AGTTAGACTCTGCTGATCTT CCTGGTAATT <u>G</u> AAT <u>C</u> ACCGCGGTT <u>T</u> CGTGGCATTGAAGATCCC GTTATTGTTGCCATTGGTGTCAAATCT	6158
		ACCGCGTG <u>A</u> TTCAATT	6159
		TAATT <u>G</u> AAT <u>C</u> ACCGCGGT	6160
		CACAAAAATGGCAACAATAACGGGATCTCAATGCCGACGAGAAC CGCGTGCTCAATT <u>A</u> GCAGGAAGATCAGCAGAGTCTAAACTGAAT TTGCCCTCAGATACTTCATAACAACCAA	6161
20	Waxy starch GBSS <i>Pisum sativum</i> Tyr18Term TAC-TAG	TTGGTTGTTATTGAAGTGTATCTGAGGCAAATT <u>C</u> AGTTAGACTCTG CTGATCTCCTTG <u>C</u> TAATTGAAGCACCGCGGTT <u>T</u> CGTGGCATTGA AGATCCCCTATTGTTGCCATTGGTGC	6162
		TTCAATT <u>A</u> GCAGGAAG	6163
		CTTCCTTG <u>C</u> TAATTGAA	6164
		TCTACACCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATT TCGTTCCAGGAGCT <u>G</u> ACACTGAGCATCCATGCATTAGAGACTAA GGCTAATAATTGTCTCACACTGGACCCCTG	6165
25	Waxy starch GBSS <i>Manihot esculenta</i> Ser14Term TCA-TGA	CAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTAATGCAT GGATGCTCAAGTGT <u>C</u> AGCTCCTGGAAACGAAATGTGCAGCTATT CAGTTGCCATGGTGTCTCTCCGGTGTAGA	6166

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CAGGAGCT <u>G</u> ACACTTGA	6167
	TCAAGTGT <u>C</u> AGCTCCTG	6168
5 Waxy starch GBSS <i>Manihot esculenta</i> Leu16Term TTG-TAG	CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTCGTT CCAGGAGCTCACACT <u>A</u> GAGCATCCATGCATTAGAGACTAAGGCTA ATAATTGTCTCACACTGGACCCCTGGACCCA TGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTA ATGCATGGATGCT <u>T</u> AGTGTGAGCTCTGGAAACGAAATGTGCAG CTATTACAGTTGCCATGGTGCTCTCCGG CTCACACT <u>A</u> GAGCATCC GGATGCT <u>T</u> AGTGTGAG	6169 6170 6171 6172
10 Waxy starch GBSS <i>Manihot esculenta</i> Leu21Term TTA-TGA	TGGCAACTGTAATAGCTGCACATTTCGTTCCAGGAGCTCACACTT GAGCATCCATGCAT <u>G</u> AGAGACTAAGGCTAATAATTGTCTCACACT GGACCCCTGGACCCAAACTATCACTCCCAA TTGGGAGTGTAGTTGGTCCAGGGTCCAGTGTGAGACAAATTAA TTAGCCTTAGTCT <u>C</u> ATGCATGGATGCTCAAGTGTGAGCTCCTGG AAACGAAATGTGCAGCTATTACAGTTGCCA CCATGCAT <u>G</u> AGAGACTA TAGTCT <u>C</u> ATGCATGG	6173 6174 6175 6176
15 Waxy starch GBSS <i>Manihot esculenta</i> Glu22Term GAG-TAG	GCAACTGTAATAGCTGCACATTTCGTTCCAGGAGCTCACACTTGA GCATCCATGCATTATAGACTAAGGCTAATAATTGTCTCACACTGG ACCCCTGGACCCAAACTATCACTCCCAAATG CATTGGGAGTGTAGTTGGTCCAGGGTCCAGTGTGAGACAAAT TATTAGCCTTAGTCT <u>A</u> ATGCATGGATGCTCAAGTGTGAGCTCCT GGAAACGAAATGTGCAGCTATTACAGTTGC ATGCATT <u>A</u> GACTAAG CTTAGTCT <u>A</u> ATGCAT	6177 6178 6179 6180
20 Waxy starch GBSS <i>Manihot esculenta</i> Lys24Term AAG-TAG	GTAATAGCTGCACATTTCGTTCCAGGAGCTCACACTTGAGCATCC ATGCATTAGAGACT <u>T</u> AGGCTAATAATTGTCTCACACTGGACCCCTG GACCCAAACTATCACTCCCAAATGGTTAA TTAACCAATTGGGAGTGTAGTTGGTCCAGGGTCCAGTGTGAG ACAAATTATTAGCCT <u>A</u> GTCTCAATGCATGGATGCTCAAGTGTGA GCTCCTGGAAACGAAATGTGCAGCTATTAC TAGAGACT <u>T</u> AGGCTAAT ATTAGCCT <u>A</u> GTCTCTA	6181 6182 6183 6184

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Phaseolus vulgaris</i> Ser12Term TCA-TGA	ACAACTCCTCCGTACCGGTATAAGCATGGCAACGGTATCGATGG CATCGTGGTGGCGT <u>GAAAAGGCCGTGGAGTACAGAGACAAAAA</u> GTGAAATCTCGGGTCAGATGAGCCTGAACCG	6185
	CGGTTCAGGCTCATCTGACCCGAAGATTCACTTTGTCTGTAC TCCACGCCCTTT <u>CACGCCACGCACGATGCCATCGATACCGTTG</u> CCATGCTTATAACCGGTGACGGAGGAGTTGT	6186
	CGTGGCGT <u>GAAAAGGCG</u>	6187
	CGCCTTT <u>CACGCCACG</u>	6188
10 Waxy starch GBSS <i>Phaseolus vulgaris</i> Trp16Term TGG-TGA	CACCGGTATAAGCATGGCAACGGTATCGATGGCATT <u>CGTGC</u> GTCAAAAGGCGCGT <u>GAA</u> GTACAGAGACAAAAGTGAATCTCGGG TCAGATGAGCCTGAACCGTCATGAATTGAAA	6189
	TTCAATT <u>CATGACGGTT</u> CAGGCTCATCTGACCCGAAGATTCACT TTTGTCTCTGTACT <u>T</u> ACGCC <u>C</u> TTTGACGCCACGCACGATGCC ATCGATACCGTTGCCATGCTTACCGGTG	6190
	GGCGCGT <u>GAA</u> GTACAGA	6191
	TCTGTACT <u>T</u> ACGCCGCC	6192
	ATAAGCATGGCAACGGTATCGATGGCATT <u>CGTGC</u> GGCGCGTGGAGTACATAGACAAAAGTGAATCTCGGGTCAGATG AGCCTGAACCGTCATGAATTGAAATACGATG CATCGTATT <u>CAATT</u> CATGACGGTT <u>CAGGCT</u> CATCTGACCCGAAGA TTTCACTTTGTCT <u>ATG</u> TACTCCACGCC <u>C</u> TTTGACGCCACGCAC GATGCCATCGATACCGTTGCCATGCTTAT GGAGTAC <u>ATAGACAAAA</u>	6193 6194 6195 6196
15 Waxy starch GBSS <i>Phaseolus vulgaris</i> Glu19Term GAG-TAG	ATGGCAACGGTATCGATGGCATT <u>CGTGC</u> GTGGAGTACAGAGACAT <u>AAGTGA</u> ATCTCGGGTCAGATGAGCCT GAACCGTCATGAATTGAAATACGATGGGTGA	6197
	TCAACCCATCGTATT <u>CAATT</u> CATGACGGTT <u>CAGGCT</u> CATCTGACC CGAAGATT <u>CACTT</u> <u>ATG</u> TCTCTGTACTCCACGCC <u>C</u> TTTGACGCC ACGCACGATGCCATCGATACCGTTGCCAT	6198
	CAGAGAC <u>ATAGTGA</u> AA	6199
	TTTC <u>CACTT</u> <u>ATG</u> TCTCTG	6200
	ACGGTATCGATGGCATT <u>CGTGC</u> TACAGAGACAAAAGT <u>GT</u> <u>TA</u> ATCTCGGGTCAGATGAGCCTGAACCG TCATGAATTGAAATACGATGGGTGAGAT <u>CTC</u> GAGATCTCAACCCATCGTATT <u>CAATT</u> CATGACGGTT <u>CAGGCT</u> CAT CTGACCCGAAGATT <u>AC</u> ACTTTGTCTGTACTCCACGCC <u>C</u> TTTGACGCCACGATGCCATCGATACCGT	6201 6202

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	CAAAAGTGTAAATCTTCG	6203
	CGAAGATT <u>A</u> CACTTTG	6204
	GCGCCTAGCTCGAAAAGGTCGTCAATTGAGAGGCTGCACCAATGG GTTCCATTCTAATT <u>A</u> GTGTTCTTATCAAACAAACAGTGTGGTTCA CTGAAACTGTGCGCCTCACATCCAATTCCAG	6205
	CTGGAATTGGATGTGAGGCGACAGTTCACTGAACCAACACTGTTT GTTTGATAAGAAC <u>A</u> CTAATTAGGAATGGAACCCATTGGTGCAGCCT CTCAATGACGACCTTTGAGCTAGGCGC	6206
	CCTAATT <u>A</u> GTGTTCTTA	6207
	TAAGAAC <u>A</u> CTAATTAGG	6208
	CCTAGCTCGAAAAGGTCGTCAATTGAGAGGCTGCACCAATGGGTT CATTCTAATTATT <u>G</u> ATCTTATCAAACAAACAGTGTGGTTCACTGA AACTGTGCGCCTCACATCCAATTCCAGCAA	6209
	TTGCTGGAATTGGATGTGAGGCGACAGTTCACTGAACCAACACT GTTTGTTGATAAG <u>A</u> CTAATAATTAGGAATGGAACCCATTGGTGCA GCCTCTCAATGACGACCTTTGAGCTAGG	6210
	AATTATT <u>G</u> ATCTTATCA	6211
	TGATAAG <u>A</u> CTAATAATT	6212
10	TCGAAAAGGTCGTCAATTGAGAGGCTGCACCAATGGGTTCCATTCC TAATTATTGTTCT <u>A</u> GCAAACAAACAGTGTGGTTCACTGAAACTGT CGCCTCACATCCAATTCCAGCAATCTTGT	6213
	ACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTCACTGAACC AACACTGTTGTT <u>G</u> CTAAGAACAAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTGCA	6214
	TGTTCT <u>A</u> GCAAACAA	6215
	TTTGTTG <u>G</u> CTAAGAACAA	6216
	CGAAAAGGTCGTCAATTGAGAGGCTGCACCAATGGGTTCCATTCT AATTATTGTTCTT <u>A</u> AAACAAACAGTGTGGTTCACTGAAACTGT GCCTCACATCCAATTCCAGCAATCTTGT	6217
15	TACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTCACTGAAC CAACACTGTTGTT <u>A</u> AAAGAACAAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTGCA	6218
	GTTCTT <u>A</u> AAACAAAC	6219
	TTTGTT <u>A</u> AAAGAAC	6220
20		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Triticum aestivum</i> Ser17Term TCA-TGA	AGGCTGCACCAATGGGTTCCATTCTAATTATTGTTCTTATCAAACA AACAGTGTGGTT <u>GACT</u> GAAACTGTCGCCTCACATCCAATTCCAGC AATCTTGTAAACAATGAAGTTATGTTCT	6221
	AGGAACATAACTTCATTGTTACAAGATTGCTGGAATTGGATGTGAG GCGACAGTTTCAGT <u>CAACCAACACTGTTGTTGATAAGAACATA</u> ATTAGGAATGGAACCCATTGGTCAGCCT	6222
	TGTGGTT <u>GACT</u> GAAAC	6223
	GTTTCAGT <u>CAACCAACAA</u>	6224
10 Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG	CAGCTGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTT <u>CTAGGGCGTGAGGCCCGAGGCCGGCG</u> GATGCCGCTCTGGCATGAGGACCGTCGGAGCTA	6225
	TAGCTCCGACGGTCTCATGCCGAGAGCCGCATCCGCCGGGCTC CGGGGCCTCACGCCCT <u>AGAAACCTGACGCCGGAACCTGTCGGT</u> GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6226
	CAGGTT <u>CTAGGGCGTG</u>	6227
	CACGCCCT <u>AGAAACCTG</u>	6228
	GGTTTCCAGGGCGTGAGGCCCGGAGGCCGGGATGCCGCTC TCGGCATGAGGACCGT <u>CTGAGCTAGCGCCGCCCAACGCAAAGC</u> CGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT	6229
15 Waxy starch GBSS <i>Triticum aestivum</i> Gly46Term GGA-TGA	AGAGGCACCGCCGGGTCCC CGGGTGCCTGCCTTCCGGCTTGCCT GGGGCGGGCGCTAGCTC <u>AGACGGTCTCATGCCGAGAGCCGCATC</u> CGCCGGGCTCCGGGGCTCACGCCCTGGAAACC	6230
	GGACCGT <u>CTGAGCTAGC</u>	6231
	GCTAGCT <u>CAAGCGGTCC</u>	6232
	CGGAGCCCGGCGGATGCCGCTCTGGCATGAGGACCGTCGGAG CTAGCGCCGCCCAACG <u>TAAAGCCGAAAGCGCACCGCGGGACC</u>	6233
20 Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CGGTGGCGCGACCACCATGGAGAGGGACCGCCGGGCTCCCG GTGCGCTTCCGGCTT <u>ACGTTGGGCGCGCTAGCTCCGACGG</u> TCCTCATGCCGAGAGCCGCATCCGCCGGCTCCG	6234
	CCCCAACG <u>TAAAGCCG</u>	6235
	CCGGCTT <u>ACGTTGGGG</u>	6236
	GCGGATGCCGCTCTGGCATGAGGACCGTCGGAGCTAGCGCCG CCCCAACG <u>CAAAGCCG</u> TAAGCGCACCGCGGGACCCGGCGGTG CCTCTCCATGGTGGTGC <u>CGCCGCCACCGGAGCGCG</u>	6237
25 Waxy starch GBSS <i>Triticum aestivum</i> Lys56Term AAA-TAA	CGCCGCTGCCGGTGGCGCGACCACCATGGAGAGGGACCGCCG GGTCCC <u>CGGGCTTGCCTACCGGTTGGCGTTGGGCGCGCTAG</u> CTCCGACGGTCTCATGCCGAGAGCCGCATCCGC	6238

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Triticum aestivum</i> Glu85Term GAG-TAG	AAAGCCGGTAAGCGCAC	6239
		GTGCGCTTACCGGCTT	6240
		CTCTCCATGGTGGTGCAGGCCACCGGAGCGGGCATGAACT CGTGTTCGTCGGCGCTAGATGGCGCCCTGGAGCAAGACCGCG GCCTCGGCACGTCTCGGGGCTCCCCCAG	6241
		CTGGGGGGAGGCCCCCGAGGACGTGCGAGGCGCCGGTCTT GCTCCAGGGCGCCATCTAGGCGCCGACGAACACGAGGTTATGC CGCCGCTGCCGGTGGCGCGACCCATGGAGAG	6242
		TCGGCGCCTAGATGGCG	6243
		CGCCATCTAGGCGCCGA	6244
	Waxy starch GBSS <i>Triticum aestivum</i> Gln8Term CAG-TAG	GTCGTCTCTCGCTGCAGGTAGCCACACCCCTGCAGCGCGATGGC GGCTCTGGTCACGTCGTAGCTGCCACCTCCGGCACCGTCCTCG GCATCACCGACAGGTTCCGGCGTGCAGGTTTC	6245
		GAAAACCTGCACGCCCGAACCTGTCGGTGTGATGCCGAGGACGGTG CCGGAGGTGGCGAGCTACGACGTGACCAAGAGCCGCCATCGCGC GCGCAGGGTGTGGTACCTGCAGCGAGAGACGAC	6246
		TCACGTCGTAGCTGCC	6247
		GGCGAGCTACGACGTGA	6248
		CAGCTGCCACCTCCGGCACCGCTCTGGCATACCGACAGGTT CCGGCGTCAGGTTTTAGGGTGTGAGGCCCGGAGGCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6249
10	Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG	TCGCTCCGGTAGTCCTCATGCCGAGCGGCATCTGCCGGGCTC CGGGGCCTCACACCCATAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6250
		CAGGTTTTAGGGTGTG	6251
		CACACCCATAAAACCTG	6252
		CCCCGGAGCCCGGAGATGCCGCTGGCATGAGGACTACCG GAGCGAGCGCCGCCCGTAGCAACAAAGCCGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCCATGGTGGTGCAG	6253
		CGCGCACCAACATGGAGAGGGACCGGCCGGTCCCGCGGTGCGC TTCCGGCTTGTGCTACGGGGCGCGCTCGCTCCGGTAGTCC TCATGCCGAGCGCGCATCTGCCGGCTCCGGGG	6254
15	Waxy starch GBSS <i>Triticum aestivum</i> Lys52Term AAG-TAG	CCGCCCCGTAGCAACAA	6255
		TTGTTGCTACGGGGCGG	6256

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCGAAGTAACAAAGCCGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCATGGTGGTGCACGCCA	6257
		TGGCGCGCACCACCATGGAGAGGCACCGCCGGTCCCGCGGTG CGCTTCCGGCTTGTACTTCGGGCGCGCTCGCTCCGGTAG TCCTCATGCCGAGCGCGCATCTGCCGGCTCCG	6258
		CCCCGAAGTAACAAAGC	6259
		GCTTGTTACTTCGGGG	6260
10	Waxy starch GBSS <i>Triticum aestivum</i> Gln54Term CAA-TAA	AGCCCAGGAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA GCGCCGCCCGAAGCAATAAGCCGAAAGCGCACCGCGGAC CCGGCGGTGCCTCTCATGGTGGTGCACGCCA	6261
		CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGTCCCGCG GTGCGCTTCCGGCTTATTGCTCGGGCGCGCTCGCTCCGG TAGTCCTCATGCCGAGCGCGCATCTGCCGGCT	6262
		CGAAGCAATAAGCCGG	6263
		CCGGCTTATTGCTCG	6264
		CAGCTGCCACCTCCGGCACCGTCCTCGGCATCACGACAGGTT CCGGCGTGCAGGTTCTAGGGCGTGAGGCCCGAACCCGGCG GATGCGGCCCTCGTCATGAGGACTATCGGAGCGA	6265
15	Waxy starch GBSS <i>Triticum durum</i> Gln28Term CAG-TAG	TCGCTCCGATAGTCCTCATGACGAGGGCGCATCCGCCGGTTC CGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGAACGGTGCCGGAGGTGGCGAGCTG	6266
		CAGGTTCTAGGGCGTG	6267
		CACGCCCTAGAAACCTG	6268
		CCCCGGAACCCGGCGGATGCCGCCCTCGTCATGAGGACTATCGG AGCGAGCGCCGCCCGTAGCAAAGCCGAAAGCGCACCGCGG AGCCGGCGGTGCCTCTCATGGTGGTGCACGCCA	6269
		TGGCGCGCACCACCATGGAGAGGCACCGCCGGTCCCGCGGTG CGCTTCCGGCTTGTCTAGGGCGCGCTCGCTCCGATAGTCC TCATGACGAGGGCGCATCCGCCGGTCCGGGG	6270
20	Waxy starch GBSS <i>Triticum durum</i> Lys52Term AAG-TAG	CCGCCCCGTAGCAAAGC	6271
		GCTTGCTACGGGGCGG	6272
		CGGAACCCGGCGGATGCCGCCCTCGTCATGAGGACTATCGGAGC GAGCGCCGCCCGAAGTAAAGCCGAAAGCGCACCGCGGGAGC CGGCGGTGCCTCTCATGGTGGTGCACGCCA	6273
		CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGTCCCGCG GTGCGCTTCCGGCTTACTTCGGGCGCGCTCGCTCCGATAG TCCTCATGACGAGGGCGCATCCGCCGGTCCG	6274

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCCCGAAGTAAAGCCGG	6275
	CCGGCTTTACTTCGGGG	6276
Waxy starch GBSS <i>Triticum durum</i> Lys56Term AAA-TAA	CGGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGC CCCGAAGCAAAGCCGGTAAGCGCACCGCAGGGAGCCGGCGGTGC CTCTCCATGGTGGTGCAGGCCACGGGAGCGGGCG CGCCGCTGCCGTGGCGCACCACTGGAGAGGGACCGCCG GCTCCCGCGGTGCGCTTACCGGCTTGCTTCGGGGCGCGCTCG CTCCGATAGTCCTCATGACGAGGGCCGCATCCGC	6277
	AAAGCCGGTAAGCGCAC	6278
	GTGCGCTTACCGGCTT	6279
		6280
Waxy starch GBSS <i>Triticum durum</i> Cys64Term TGC-TGA	TATCGGAGCGAGCGCCGCCCGAAGCAAAGCCGGAAAGCGCACCG GCGGGAGCCGGCGGTGACTCTCCATGGTGGTGCAGGCCACGGG CAGCGGCGGCATGAACCTCGTGTTCGTCGGCGCC GGCCCGACGAACACGAGGTTATGCCGCCGCTGCCGTGGCG CGCACCAACATGGAGAGTACCCGCCGGCTCCCGCGGTGCGCTT CCGGCTTGCTTCGGGGCGCGCTCGCTCCGATA	6281
	CGGCGGTGACTCTCCAT	6282
	ATGGAGAGTACCCGCCG	6283
		6284
Waxy starch GBSS <i>Triticum turgidum</i> Gln28Term CAG-TAG	CAGCTGCCACCTCCGGCACCGTCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTTAGGGTGTGAGGCCCGAGCCCGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA TCGCTCCGGTAGTCCTCATGCCGAGCGGCATCTGCCGGCTC CGGGGCCTCACACCCCTAAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6285
	CAGGTTTTAGGGTGTG	6286
	CACACCCCTAAAAACCTG	6287
		6288
Waxy starch GBSS <i>Triticum turgidum</i> Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCG GAGCGAGCGCCGCCCGTAGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCCATGGTGGTGCAGCG CGCGCACCACCATGGAGAGGGACCCGCCGGTCCCGCGGTGCGC TTTCCGGCTTGTGCTACGGGGCGCGCTCGCTCCGGTAGTCC TCATGCCGAGCGGCATCTGCCGGCTCCGGGG	6289
	CCGCCCCGTAGCAACAA	6290
	TTGTTGCTACGGGGCGG	6291
		6292

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Triticum turgidum</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCACGCCA	6293
	TGGCGCGACCACCATGGAGAGGGACCGCCGGTCCCACGGT CGCTTCCGGCTTGTAACTTCGGGGCGCGCTCGCTCCGGTAG TCCTCATGCCGAGCGCGCATCTGCCGGCTCCG	6294
	CCCCGAAGTAACAAAGC	6295
	GCTTGTAACTTCGGGG	6296
10 Waxy starch GBSS <i>Triticum turgidum</i> Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA GCGCCGCCCGAAGCAATAAGCCGGAAAGCGCACCGCGGAC CCGGCGGTGCCTCTCCATGGTGGTGCACGCCA	6297
	CCGTGGCGCGACCACCATGGAGAGGGACCGCCGGTCCCACGG GTGCGCTTCCGGCTTATTGCTCAGGGCGCGCTCGCTCCGG TAGCCTCATGCCGAGCGCGCATCTGCCGGCT	6298
	CGAAGCAATAAGCCGG	6299
	CCGGCTTATTGCTCG	6300
15 Waxy starch GBSS <i>Triticum turgidum</i> Lys57Term AAA-TAA	GATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCC CGAAGCAACAAAGCCGGTAAGCGCACCGCGGACCCGGCGGT CCTCTCCATGGTGGTGCACGCCA	6301
	CGGCGCTGCCGTGGCGCGACCACCATGGAGAGGGACCGCCG GGTCCCAGGGTGCCTTACCGGCTTGTGCTTCAGGGCGCGC TCGCTCCGGTAGTCCTCATGCCGAGCGCGCATC	6302
	AAAGCCGGTAAGCGCAC	6303
	GTGCGCTTACCGGCTT	6304
20 Waxy starch GBSS <i>Aegilops speltoides</i> Gln28Term CAG-TAG	CAGCTGCCACCTCCGCCACCGCTCTCGGCATACCGACAGGTT CCGCCATGCAGGTTCTAGGGCGTGGGAGGCCGGAGCCGGCAG ATGCGCCGCTCGGCATGAGGACTGTCGGAGCGA	6305
	TCGCTCCGACAGTCCTCATGCCGAGCGCGCATCTGCCGGCTC CGGGGCCTCACGCCCTAGAAACCTGCATGGCGAACCTGTCGGT GATGCCGAGGACGGTGGCGGAGGTGGCGAGCTG	6306
	CAGGTTCTAGGGCGTG	6307
	CACGCCCTAGAAACCTG	6308
25 Waxy starch GBSS <i>Aegilops speltoides</i> Gly46Term GGA-TGA	GGTTCCAGGGCGTGGAGGCCCCGGAGCCGGCAGATGCGCCGC TCGGCATGAGGACTGTCAGAGCGAGCGCCGCCGAAGCAACAA AGCCGGAAAGCGCACCGCGGGACCCGGCGGTGCC	6309
	GGCACCGCCGGTCCCGCGGTGCCTTCCGGCTTGTGCTTC GGGGCGGGCGCTCGCTCAGACAGTCCTCATGCCGAGCGCGCAT CTGCCGGCTCCGGGCTCACGCCCTGGAAACC	6310

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGACTGTCTGAGCGAGC	6311
	GCTCGCTCAGACAGTCC	6312
5 Waxy starch GBSS <i>Aegilops speltoides</i> Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCG GAGCGAGCGCCGCCCGTAGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCGATGGTGGTGCACG	6313
	CGCGCACCAACCATCGAGAGGCACCGCCGGTCCCGCGGTGC TTCCGGCTTGTGCTACGGGGCGCGCTCGCTCCGACAGTCC TCATGCCGAGCGGCCATCTGCCGGCTCCGGGG	6314
	CCGCCCCGTAGCAACAA	6315
	TTGTTGCTACGGGGCGG	6316
	CGGAGCCCGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAG CGAGCGCCGCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCGATGGTGGTGCACG	6317
10 Waxy starch GBSS <i>Aegilops speltoides</i> Gln53Term CAA-TAA	TGGCGCGCACCAACCATCGAGAGGCACCGCCGGTCCCGCGGTG CGCTTCCGGCTTGTGCTACCTCGGGCGCGCTCGCTCCGACAG TCCTCATGCCGAGCGGCCATCTGCCGGCTCCG	6318
	CCCCGAAGTAACAAAGC	6319
	GCTTGTGTTACTTCGGGG	6320
	AGCCCCGGCAGATGCCGCCCTCGGCATGAGGACTGTCGGAGCGA GCGCCGCCCGAAGCAATAAGCCGGAAAGCGCACCGCGGGAC CCGGCGGTGCCTCTCGATGGTGGTGCACG	6321
	CGGTGGCGCGCACCAACCATCGAGAGGCACCGCCGGTCCCGCG GTGCGCTTCCGGCTTATTGCTCGGGCGCGCTCGCTCCGA CAGTCCTCATGCCGAGCGGCCATCTGCCGGCT	6322
15 Waxy starch GBSS <i>Aegilops speltoides</i> Gln54Term CAA-TAA	CGAAGCAATAAGCCGG	6323
	CCGGCTTATTGCTTCG	6324
	AGTGCAGAGATCTTCCACAGCAACAGCTAGACAACCACATGTCG GCTCTCACACAGTCTAGCTGCCACCTCGGCCACCGCTTCGG CATCGCTGACAGGTGGCGCCGTCGCTGC	6325
	GCAGCGACGACGGCGCCGACCTGTCAGCGATGCCGAAGCCGGT GCCCGAGGTGGCGAGCTAGGACGTGGTGAAGAGCCGACATGGT GTTGTCTAGCTGTTGCTGTGGAAGATCTCGACT	6326
	CCACGTCTAGCTGCC	6327
20 Waxy starch GBSS <i>Oryza glaberrima</i> Gln8Term CAG-TAG	GGCGAGCTAGGACGTGG	6328

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Waxy starch GBSS <i>Oryza glaberrima</i> Ser12Term TCG-TAG	TCCACAGCAACAGCTAGACAACCACCATGTCGGCTCTCACCACT CCCAGCTGCCACCT <u>A</u> GGCCACCGGCTCGGCATCGCTGACAGG TCGGCGCCGTCGTCGCTGCTCCGCCACGGGTT	6329
		AACCCGTGGCGGAGCAGCGACGACGGCGCCGACCTGTCAGCGAT GCCGAAGCCGGTGGCT <u>A</u> GGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA	6330
		CGCCACCT <u>A</u> GGCCACCG	6331
		CGGTGGCCT <u>A</u> GGTGGCG	6332
10	Waxy starch GBSS <i>Oryza glaberrima</i> Ser22Term TCG-TAG	CGGCTCTACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCTGACAGGT <u>A</u> GGCGCCGTCGCTGCTCCGCCACGG GTTCCAGGGCCTCAAGCCCCGAGCCCCGCCGG	6333
		CCGGCGGGGCTGCGGGGCTT <u>A</u> GGGCCCTGGAACCGTGGCGGA GCAGCGACGACGGCGCT <u>A</u> CCCTGTCAGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6334
		TGACAGGTA <u>GGCGCCGT</u>	6335
		ACGGCGCCT <u>A</u> CCGTGCA	6336
		CCACGTCCCAGCTGCCACCTCGGCCACCGGCTTCGGCATCGCT GACAGGTCGGCGCCGT <u>A</u> GTGCGCTGCTCCGCCACGGGTTCCAGG GCCTCAAGCCCCGAGCCCCGCCGGCGACGC	6337
15	Waxy starch GBSS <i>Oryza glaberrima</i> Ser25Term TCG-TAG	CGTGCGCCGCCGGCGGGCTGCGGGGCTT <u>A</u> GGGCCCTGGAACC CGTGGCGAGCAGCGACT <u>A</u> CCGCGCCGACCTGTCAGCGATGCC GAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG GGCGCCGT <u>A</u> GTGCGCTGC	6338
		GCAGCGACT <u>A</u> CCGGGCC	6339
		CGTCCCAGCTGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC AGGTGGCGCCGT <u>A</u> GTGCGCTGCCACGGGTTCCAGGGCCT CAAGCCCCGAGCCCCGCCGGCGACGC	6341
		GTGCGTCGCCGCCGGCGGGCTGCGGGGCTT <u>A</u> GGGCCCTGGA ACCCGTGGCGAGCAGCT <u>A</u> CGACGGCGCCGACCTGTCAGCGATG CCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGG	6342
20	Waxy starch GBSS <i>Oryza glaberrima</i> Ser26Term TCG-TAG	GCCGTCGT <u>A</u> GTGCTCC	6343
		GGAGCAGCT <u>A</u> CGACGGC	6344
		TCCACAGCAAGAGCTAACAGCCGACCGTGTGCACCACCATGTCG GCTCTCACCACT <u>A</u> GGCTGCCACCTCGGCCACCGGCTTCGG CATCGCCGACAGGTGGCGCCGACCTGTCGGCATGCCAAGCCGGT	6345
25	Waxy starch GBSS <i>Oryza sativa</i> Gln8Term CAG-TAG	GCAGCGACGACGGCGCCGACCTGTCGGCATGCCAAGCCGGT GGCCGAGGTGGCGAGCT <u>A</u> GGACGTGGTGAGAGCCGACATGGTG GTGCACACGGTCGGCTGTTAGCTTGTGGA	6346

	Phenotype: Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
		CCACGTCC <u>T</u> AGCTCGCC	6347
		GGCGAGCT <u>A</u> GGACGTGG	6348
5	Waxy starch GBSS <i>Oryza sativa</i> Ser12Term TCG-TAG	CTAACAGCCGACCGTGTGCACCACCATGTCGGCTCTCACCACT CCCAGCTGCCACCT <u>A</u> GGCCACCGGCTTCGGCATGCCGACAGG TCGGCGCCGTCGCTGCTTCGCCACGGGTT	6349
		AACCCGTGGCGAAGCAGCGACGACGGGCCGACCTGTGGCGAT GCCGAAGCCGGTGGC <u>T</u> AGGTGGCGAGCTGGACGTGGTGAGA GCCGACATGGTGGCACACGGTCGGCTGTTAG	6350
		CGCCACCT <u>A</u> GGCCACCG	6351
		CGGTGGC <u>T</u> AGGTGGCG	6352
		CGGCTCTACCACGTCCAGCTGCCACCTCGGCCACCGGCTTC GGCATGCCGACAG <u>T</u> AGGCGCCGTCGCTGCTTCGCCACGG GTTCCAGGGCCTCAAGCCCCGTAGCCCAGCCGG	6353
10	Waxy starch GBSS <i>Oryza sativa</i> Ser22Term TCG-TAG	CCGGCTGGGCTACGGGGCTTGAGGCCCTTGAACCCGTGGCGAA GCAGCGACGACGGGCC <u>T</u> ACCTGTGGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6354
		CGACAGGT <u>A</u> GGCGCCGT	6355
		ACGGCGC <u>T</u> ACCTGTGCG	6356
		CCACGTCCAGCTGCCACCTCGGCCACCGGCTTCGGCATGCC GACAGGTGGCGCC <u>T</u> AGTCGCTGCTTCGCCACGGGTTCCAGGG CCTCAAGCCCCGTAGCCCAGCCGGGGACGC	6357
		CGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAAACC CGTGGCGAAGCAG <u>C</u> ACTACGGGCCACCTGTGGCGATGCC GAAGCCGGTGGCGAGGTGGCGAGCTGGGACGTGG	6358
15	Waxy starch GBSS <i>Oryza sativa</i> Ser25Term TCG-TAG	GGCGCCGT <u>A</u> GTGCTGCG	6359
		GCAGCGACT <u>A</u> CGGCC	6360
		CGTCCCAGCTGCCACCTCGGCCACCGGCTTCGGCATGCCGAC AGGTGGCGCCGT <u>T</u> AGCTGCTTCGCCACGGGTTCCAGGGCCT CAAGCCCCGTAGCCCAGCCGGGGACGCATC	6361
		GATGCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAA CCC GTGGCGAAGCAG <u>C</u> ACTACGACGGGCCACCTGTGGCGATGC CGAAGCCGGTGGCGAGGTGGCGAGCTGGGACG	6362
		GGCGTCG <u>T</u> AGCTGCTTC	6363
20	Waxy starch GBSS <i>Oryza sativa</i> Ser26Term TCG-TAG	GAAGCAG <u>C</u> ACGACGGC	6364

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Hordeum vulgare</i> Gln8Term CAG-TAG	GTCTCTCACTGCAGGTAGCCACACCCCTGTGCGCGGCCATGGC GGCTCTGCCACGTCTAGCTGCCACCTCCGGCACCGTCTCG GCGTCACCGACAGATTCCGGCGTCCAGGTTTC	6365
		GAAAACCTGGACGCCGAATCTGCGGTGACGCCGAGGACGGT CCGGAGGTGGCGAGCTAGGACGTGGCCAGAGCCGCCATGGCG CGCGCACAGGGTGTGGTACCTGCAGTGAGAGAC	6366
		CCACGTCTAGCTGCC	6367
		GGCGAGCTAGGACGTGG	6368
		ATGGCGGCTCTGGCCACGTCCCAGCTGCCACCTCCGGCACCGT CCTCGGCGTCACCGACTGATTCCGGCGTCCAGGTTTCAGGGCCT CAGGCCCGGAACCCGGCGGATGCCGGCTT	6369
10	Waxy starch GBSS <i>Hordeum vulgare</i> Arg21Term AGA-TGA	CAAGCGCCGATCCGCCGGGTTCCGGGGCTGAGGCCCTGAAAA CCTGGACGCCGGAATCAGTCGGTGACGCCGAGGACGGTGCGG AGGTGGCGAGCTGGGACGTGGCCAGAGCCGCCAT	6370
		TCACCGACTGATTCCGG	6371
		CCGGAATCAGTCGGTGA	6372
		CAGCTGCCACCTCCGGCACCGTCCTCGCGTCACCGACAGATT CCGGCGTCCAGGTTTAAAGGGCTCAGGCCCGGAACCCGGCG ATGCGCGCTTGGTATGAGGACTATCGGAGCAA	6373
		TTGCTCCGATAGTCCTCATACCAAGCGCCGATCCGCCGGGTTCC GGGGCCTGAGGCCCTAAAAACCTGGACGCCGGAATCTGCGGT ACGCCGAGGACGGTGCCTGGAGGTGGCGAGCTG	6374
15	Waxy starch GBSS <i>Hordeum vulgare</i> Gln28Term CAG-TAG	CAGGTTTAAAGGGCTC GAGGCCCTAAAAACCTG	6375 6376
		GGTTTCAGGGCTCAGGCCCGGAACCCGGCGATGCCGCT TGGTATGAGGACTATCTGAGCAAGCGCCGCCGAAGCAAAGCC GGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCT	6377
		AGAGGCACCGCCGGCTCCCGCGGTGCCTTCCGGTTGCTT GGGGCGCGCTTGCCTAGATAGTCCTCATACCAAGCGCCGCATC CGCCGGGTTCCGGGCCCTGAGGCCCTGAAAACC	6378
		GGACTATCTGAGCAAGC GCTTGCTCAGATAGTCC	6379 6380
		CCCCGGAACCGGGCGGATGCCGCGCTTGGTATGAGGACTATCGG AGCAAGCGCCGCCCGTAGCAAAGCCGAAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCGTGGTGGTGGCGCCA	6381
20	Waxy starch GBSS <i>Hordeum vulgare</i> Gly46Term GGA-TGA	TGGCGCTCACCACCAACGGAGAGGCACGCCGGCTCCCGCGT CGCTTCCGGCTTGTCAAGGGGGCGGCCCTGCTCCGATAGTCC TCATACCAAGCGCCGCATCCGCCGGTTCCGGGG	6382
25	Waxy starch GBSS <i>Hordeum vulgare</i> Lys52Term AAG-TAG		

	Phenotype, Gene, Plant, & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Waxy starch GBSS <i>Zea mays</i> Gln8Term CAG-TAG	CCGCCCCGTAGCAAAGC	6383
		GCTTGCTACGGGGCGG	6384
		ACGTCTTTCTCTCTCCTACGGCAGTGGATTAATCGGCATGGCGG CTCTGGCCACGTCGTAGCTCGTCGCAACCGCGCCGGCCTGGC GTCCCGGACCGTCCACGTTCCGCCGCGCG	6385
		CGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCAGGCC GCGCGTTGCGACGAGCTACGACGTGGCCAGAGCCGCCATGCCGA TTAATCCACTGCGTAGGAGAGAGAGAAAAGACGT	6386
		CCACGTCGTAGCTCGTC	6387
		GACGAGCTACGACGTGG	6388
	Waxy starch GBSS <i>Zea mays</i> Gln30Term CAG-TAG	GTCGCAACCGCGGCCGGCTGGCGTCCGGACGGTCCACGT TCCGCCGCGGCGCCCGCGTAGGGCCTGAGGGGGGCCCGGGCGTC GGCGCGGGCGGACACGCTCAGCATGCGGACCAGCG	6389
		CGCTGGTCCGCATGCTAGCGTGTCCGCCGCCGACGCCG GGCCCCCCTCAGGCCCTACGCGCGCCGCCGGAACGTGGAC GCGTCCGGGACGCCAGGCCGGCGCGTGTGCGAC	6390
		GCGCCGCGTAGGGCCTG	6391
		CAGGCCCTACGCGGCCG	6392
		TCCCGGACCGTCCACGTTCCGCCGCCGGCCGCCAGGGCCT GAGGGGGGCCCGGGCGTAGGGCGGGGACACGCTCAGCATG CGGACCGCGCGCGCGCCAGGCACCAGCA	6393
10	Waxy starch GBSS <i>Zea mays</i> Ser38Term TCG-TAG	TGCTGGTGCCTGGCGCCGCGCGCTGGTCCGCATGCTGA GCGTGTCCGCCGCCCTACGCCGGGCCCCCTCAGGCCCTG CGCGCGCCGCCGGCGGAACGTGGACGCGTCCGGGA	6394
		CCGGGCGTAGGGCGCGG	6395
		CCGCCGCCTACGCCCGG	6396
		GCGTCGGCGGGCGGACACGCTCAGCATGCGGACCAGCGCGC GCGCGCGCCCAGGCCACTAGCAGCAGGCCGCCGGGGCA GGTTCCCGTCGCTCGTGTGCGCCAGCGCCGGCA	6397
		TGCCGGCGCTGGCGCACACGACGAGCGACGGGAACTGCCCC GCGCGGCCCTGCTGCTAGTGCCTGGCGCCGCCGCGCTG GTCCGCATGCTGAGCGTGTCCGCCGCCGACGC	6398
15	Waxy starch GBSS <i>Zea mays</i> Ser57Term CAG-TAG	CCAGGCACACTAGCAGCAG	6399
		CTGCTGCTAGTGCCTGG	6400

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Zea mays</i> Gln58Term CAG-TAG	TCGGCGGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCG CGGCGCCCAGGCACCA <u>G</u> TAGCAGGCGCCGGGGCAGGTT CCCGTCGCTCGTCGTGCGCCAGCGCCGGCATGA	6401
	TCATGCCGGCGCTGGCGCACACGACGAGCGACGGGAAACCTGCC CCGCGGCGCGCCTG <u>C</u> T <u>A</u> CTGGTGCTGGCGCCGCGCGC TGGTCCGCATGCTGAGCGTGTCCGCCGCCGA	6402
	GGCACCA <u>G</u> TAGCAGGCG	6403
	CGCCTGCT <u>A</u> CTGGTGCC	6404

**Example 11****Altering fatty acid content of plants**

Improved means to manipulate fatty acid compositions, from biosynthetic or natural plant sources, are needed. For example, oils containing reduced saturated fatty acids are desired for dietary reasons and oils containing increased saturated fatty acids are also needed as alternatives to current sources of highly saturated oil products, such as tropical oils or chemically hydrogenated oils. It would therefore be advantageous to influence directly the production and composition of fatty acids in crop plants.

Higher plants synthesize fatty acids, primarily palmitic, stearic and oleic acids, in the plastids (i.e., chloroplasts, proplastids, or other related organelles) as part of the Fatty Acid Synthase (FAS) complex. Fatty acid synthesis is the result of the three enzymatic activities: acyl-ACP elongase, acyl-ACP desaturase and acyl-ACP thioesterases specific for each of palmitoyl-, stearoyl- and oleoyl-ACP.

A variety of enzymes have been identified that influence the relative levels of saturated vs. unsaturated fatty acids in plants. For example, the enzymes stearoyl-acyl carrier protein (stearoyl-ACP) desaturase, oleoyl desaturase and linoleate desaturase produce unsaturated fatty acids from saturated precursors. Similarly, relative enzymatic activities of the various acyl-ACP thioesterases influences the relative acyl-chain composition of the resultant fatty acids. Consequently a reduction or an increase of the activity of these enzymes can alter the properties of oils produced in a plant. In fact, specific targeting of particular enzymatic activities can results in altered levels of particular fatty acids.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes encoding proteins involved in fatty acid biosynthesis.

**Table 22**  
**Oligonucleotides to produce plants with reduced palmitate**

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser8Term TCG-TAG	TTTGGTGGCAGTGTCTTGAACGCTTCATCTCCTCGTCATGGTGGC CACCTCTGCTACGTAGTCATTCTTCTGTACCATCTTCTTCACTT GATCCTAATGGAAAAGGCAATAAGATTGG CCAATCTTATTGCCTTCCATTAGGATCAAGTGAAGAAGATGGTA CAGGAAAGAATGACTACGTAGCAGAGGGTGGCCACCATGACGAGG AGATGAAGCGTTCAAAGACACTGCCACCAAA	6405 6406

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser9Term TCA-TGA	TGCTACGT <u>A</u> GTCAATTCT	6407
		AGAATGACT <u>A</u> CGTAGCA	6408
		GGTGGCAGTGTCTTGAAACGCTTCATCTCCTCGTCATGGTGGCCA CCTCTGCTACGT <u>G</u> ATTCTTCCTGTACCATCTTCACTTGAT CCTAATGGAAAAGGCAATAAGATTGGGTC	6409
		GACCAATCTTATTGCCTTTCCATTAGGATCAAGTGAAGAAGATG GTACAGGAAAAGAAT <u>C</u> ACGACGTAGCAGAGGTGGCCACCATGACGA GGAGATGAAGCGTTCAAAGACACTGCCACC	6410
		TACGT <u>C</u> GT <u>G</u> ATTCTTC	6411
		GAAAGAAC <u>T</u> ACGACGTA	6412
	Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser17Term TCA-TGA	ATCTCCTCGTCATGGTGGCCACCTCTGCTACGT <u>C</u> GTCAATTCTTC TGTACCATCTT <u>C</u> TT <u>G</u> ACTTGATCCTAATGGAAAAGGCAATAAGATT GGGTCTACGAATCTTGCTGGACTCAATT	6413
		GAATTGAGTCCAGCAAGATT <u>C</u> GTAGACCCAATCTTATTGCCTTT CATTAGGATCAAGT <u>C</u> AAGAAGATGGTACAGGAAAGAATGACGACG TAGCAGAGGTGGCCACCATGACGAGGAGAT	6414
		ATCTTCTT <u>G</u> ACTTGATC	6415
		GATCAAGT <u>C</u> AAGAAGAT	6416
		GTGGCCACCTCTGCTACGT <u>C</u> GTCAATTCTTCCTGTACCATCTT CACTTGATCCTAAT <u>T</u> GGAAAAGGCAATAAGATTGGGTCTACGAATCT TGCTGGACTCAATTCTGCACCTA <u>ACT</u> CTG CAGAGTTAGGTGCAGAATTGAGTCCAGCAAGATT <u>C</u> GTAGACCCAATCTTATTGCCTTT <u>C</u> ATTAGGATCAAGTGAAGAAGATGGTACAGG AAAGAAC <u>T</u> GACGACGTAGCAGAGGTGGCCAC	6417
10	Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Gly22Term GGA-TGA	ATCCTAATT <u>T</u> GGAAAAGGC	6418
		GCCTTT <u>C</u> ATTAGGAT	6419
		GCTTGAATT <u>T</u> GTGATCTGATTGGTAATTGTGGCCACAATGGTGCTACTGCCGACCG <u>T</u> ATCATTCTTCGTTGACTTCCCCTCTGGG GATGCCAAATCGGGCAATCCCGGAAAAGG	6420
		CCTTTCCGGGATTGCCGATTGGCATCCCCAGAACGGGAAGTC AACGGAAAAGAAC <u>T</u> GAT <u>C</u> ACGTGGCGCAGTAGCAACCATTGTGGCC ACAATTAA <u>CC</u> ATCAGATCACAAATTCAAGC CGCCACGT <u>T</u> ATCATTCT	6421
		AGAATGAT <u>C</u> ACGTGGCG	6422
15	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser8Term TCA-TGA	CGCCACGT <u>T</u> ATCATTCT	6423
		AGAATGAT <u>C</u> ACGTGGCG	6424
		GCTTGAATT <u>T</u> GTGATCTGATTGGTAATTGTGGCCACAATGGTGCTACTGCCGACCG <u>T</u> ATCATTCTTCGTTGACTTCCCCTCTGGG GATGCCAAATCGGGCAATCCCGGAAAAGG	6421
		CCTTTCCGGGATTGCCGATTGGCATCCCCAGAACGGGAAGTC AACGGAAAAGAAC <u>T</u> GAT <u>C</u> ACGTGGCGCAGTAGCAACCATTGTGGCC ACAATTAA <u>CC</u> ATCAGATCACAAATTCAAGC CGCCACGT <u>T</u> ATCATTCT	6422
		AGAATGAT <u>C</u> ACGTGGCG	6423

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser9Term TCA-TGA	TGAATTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTAC TGCCGCCACGT <del>CATGATTCTTCCGTTGACTTCCCCTCTGGGGAT</del> GCCAAATCGGGCAATCCCGAAAAGGGTC GACCCTTTCCGGGATTGCCGATTGGCATCCCCAGAAGGGGAA GTCAACGGAAAGAACATGACGTGGCGGAGTAGCAACCATTGTG GCCACAATTAAACCAATCAGATCACAAATTCA CACGT <del>CATGATTCTTC</del> GAAAGAACATGACGTG	6425 6426 6427 6428
		CTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT CATCATTCTTCCGT <del>A</del> GACTTCCCCTCTGGGGATGCCAAATCGG GCAATCCCGAAAAGGGTCGGTGAGTTTGG	6429
		CCAAA <del>ACT</del> CACCGACCC <del>TTT</del> CCGGGATTGCCGATTGGCATCC CCAGAAGGGGAAGTCTACGGAAAGAACATGATGACGTGGCGGAGT AGCAACCATTGTGGCCACAATTAAACCAATCAG CTTCCGT <del>A</del> GACTTCCC	6430 6431
		GGGAAGTCTACGGAAAG	6432
10	Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Leu13Term TTG-TAG	ATGGTTGCTACTGCCGCCACGT <del>CATCATTCTTCCGTTGACTTCCC</del> CTTCTGGGGATGCC <del>T</del> ATCGGGCAATCCCGAAAAGGGTCGGTG AGTTTGGGTCAATGAAGTCGAAATCCGCGG	6433
		CCCGGGATT <del>CGACTT</del> CATTGACCCAAA <del>ACT</del> CACCGACCC <del>TTT</del> CC GGGATTGCCCGATT <del>A</del> GGCATCCCCAGAAGGGGAAGTCAACGGAA AGAATGATGACGTGGCGGAGTAGCAACC <del>AT</del>	6434
		GGGATGCC <del>T</del> ATCGGGC GCCCGATT <del>A</del> GGCATCCC	6435 6436
		GGGATT <del>CGACAT</del> GGGATGGCCTATGTCAACAGCAGTAGCAACC <del>ATGGTTT</del> TA AAAACA <del>ACTTCAATT</del> TCGTGCTGAAATCCC TGTGACAT <del>A</del> GGCGTTT AAAACGCC <del>T</del> ATGTCA	6437 6438 6439 6440
15	Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser8Term TCG-TAG	GGGATT <del>CGACAA</del> TTGAAG <del>TTGTTT</del> AAAACC <del>ATGGTTGC</del> TACTGCTGTGACAT <del>A</del> GGCGTTT <del>CC</del> AGTC <del>ACTT</del> CTCAC <del>CT</del> GAC TCCCTGACTCGAAAAACAAGAACGCTCGG	6437
		CCGAGCTTGT <del>TTGTTT</del> CGAGTCAGAGGAGTCAGGTGAAGAAGTG ACTGGGAAAAACGCC <del>T</del> ATGT <del>CACAGCAGTAGCAACC</del> ATGGTTTTA AAAACA <del>ACTTCAATT</del> TCGTGCTGAAATCCC TGTGACAT <del>A</del> GGCGTTT AAAACGCC <del>T</del> ATGTCA	6438 6439 6440
		TGT <del>TTT</del> AAAACC <del>ATGGTTGCTACTGCTGTGACATCGGC</del> TTT CCCAGTC <del>ACTT</del> CTGAC <del>CT</del> CCTCTGACTCGAAAAACAAGAACG CTCGGAAGCATCAAGTCGAAGGCCATCGGT	6441
		ACCGATGGCTTCGACTT <del>GATGCT</del> CCGAGC <del>TTCTGTTT</del> CGAGT CAGAGGAGTCAGGT <del>CAAGAAGT</del> GACTGGAAAAACGCCATGTCA CAGCAGTAGCAACC <del>ATGGTTT</del> AAAACA	6442
20	Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser16Term TCA-TGA	TGT <del>TTT</del> AAAACC <del>ATGGTTGCTACTGCTGTGACATCGGC</del> TTT CCCAGTC <del>ACTT</del> CTGAC <del>CT</del> CCTCTGACTCGAAAAACAAGAACG CTCGGAAGCATCAAGTCGAAGGCCATCGGT	6441
		ACCGATGGCTTCGACTT <del>GATGCT</del> CCGAGC <del>TTCTGTTT</del> CGAGT CAGAGGAGTCAGGT <del>CAAGAAGT</del> GACTGGAAAAACGCCATGTCA CAGCAGTAGCAACC <del>ATGGTTT</del> AAAACA	6442
25	Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser16Term TCA-TGA	TGT <del>TTT</del> AAAACC <del>ATGGTTGCTACTGCTGTGACATCGGC</del> TTT CCCAGTC <del>ACTT</del> CTGAC <del>CT</del> CCTCTGACTCGAAAAACAAGAACG CTCGGAAGCATCAAGTCGAAGGCCATCGGT	6441
		ACCGATGGCTTCGACTT <del>GATGCT</del> CCGAGC <del>TTCTGTTT</del> CGAGT CAGAGGAGTCAGGT <del>CAAGAAGT</del> GACTGGAAAAACGCCATGTCA CAGCAGTAGCAACC <del>ATGGTTT</del> AAAACA	6442

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CACTTCTT <u>GACCTGACT</u>	6443
	AGTCAGGT <u>CAAGAAGTG</u>	6444
5 Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser22Term TCG-TAG	TTGCTACTGCTGTGACATGGCGTTTTCCCACTCACTTCTCACC TGACTCCTCTGACT <u>AGAAAAACAAGAAGCTCGGAAGCATCAAGTC</u> GAAGCCATCGGTTCTCTGGAAAGTTTGCA	6445
	TGCAAACCTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCGA GCTTCTTGT <u>TTCTAGTCAGAGGAGTCAGGTGAAGAAGTACTGG</u> GAAAAACGCCGATGTACAGCAGTAGCAA	6446
	CTCTGACT <u>AGAAAAACA</u>	6447
	TGTTTTCT <u>AGTCAGAG</u>	6448
	GCTACTGCTGTGACATGGCGTTTTCCCACTCACTTCTCACCTG ACTCCTCTGACT <u>CGTAAAACAAGAAGCTCGGAAGCATCAAGTCGA</u> AGCCATCGGTTCTCTGGAAAGTTGCAAG	6449
10 Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Lys23Term AAA-TAA	CTTGCAAACCTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCC GAGCTTCTTGT <u>TTACGAGTCAGAGGAGTCAGGTGAAGAAGTAC</u> TGGGAAAAACGCCGATGTACAGCAGTAGC	6450
	CTGACTCG <u>TTAAACAAG</u>	6451
	CTTGT <u>TTTACGAGTCAG</u>	6452
	CTCCCGCTCG <u>TTGAAAGACAATGGTGGCTACCGCTGCAAGCTCTG</u> CATTCTTCCCCGTGT <u>AGTCCCCGGTCACCTCCTAGACCAGGAA</u> AGCCCGGAAATGGGT <u>CATCGAGCTTCAGCCC</u>	6453
	GGGCTGAAGCTCGAT <u>GACCCATTCCGGGTTCTGGTAGAG</u> GAGGTGACC <u>GGGGACTACACGGGAAGAATGCAGAGCTTGCAGC</u> GGTAGCCACCATTGT <u>CTTCAACGAGCGGGAG</u>	6454
15 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Ser14Term TCG-TAG	CCCCGTGT <u>AGTCCCCGG</u>	6455
	CCGGGG <u>ACTACACGGGG</u>	6456
	ATGGTGGCTACCGCTGCAAGCTCTGCATTCTCCCGTGT <u>CGTCC</u> CCGGTCACCTCCT <u>CTTGACCAGGAAAGCCCGGAAATGGGT</u> CATCG AGCTTCAG <u>CCCCATCAAGCCAAATTGT</u> CG	6457
	CGACAAATT <u>GGGCTTGATGGGGCTGAAGCTCGATGACCCATT</u> C CGGGCTT <u>CTGGTCAAGAGGAGGTGACCGGGGACGACACGGG</u> GAAGAAT <u>GCAGAGCTTGCAGCGTAGCCACCAT</u>	6458
	CCTCCT <u>CTTGACCAGGA</u>	6459
20 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Arg21Term AGA-TGA	TCCTGGT <u>CAAGAGGAGG</u>	6460

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gly23Term GGA-TGA	GCTACCGCTGCAAGCTCTGCATTCTCCCCGTGTCGTCCCCGGTC ACCTCCTCTAGACCA <u>TGAAAGCCCGGAAATGGGT</u> CATCGAGCTTC AGCCCCATCAAGCCCAAATTGTCGCCAATG	6461
		CATTGGCGACAAATTGGGCTT <u>GATGGGCTGAAAGCTCGATGACC</u> CATTCCGGGCTTC <u>ATGGTCTAGAGGAGGTGACCGGGGACGAC</u> ACGGGGAAGAATGCAGAGCTTGCAGCGGTAGC	6462
		CTAGACCA <u>TGAAAGCCC</u>	6463
		GGGCTT <u>TCATGGTCTAG</u>	6464
10	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG	ACCGCTGCAAGCTCTGCATTCTCCCCGTGTCGTCCCCGGTCACC TCCTCTAGACCA <u>GGGAAATGGGT</u> CATCGAGCTTCAGC CCCATCAAGCCCAAATTGTCGCCAATGGCG	6465
		CGCCATTGGCGACAAATTGGGCTT <u>GATGGGCTGAAAGCTCGATG</u> ACCCATTCCGGGCT <u>ATCCTGGTCTAGAGGAGGTGACCGGGGAC</u> GACACGGGGAAGAATGCAGAGCTTGCAGCGGT	6466
		GACCAGGA <u>AGCCCCGA</u>	6467
		TCGGGCT <u>ATCCTGGTC</u>	6468
		GCCACCGCTGCAAGTTCTGCATTCTCCCCCTGCCGTCCCCGGAC ACCTCCTCTAGGCCG <u>TGAAAGCTCGGAAATGGGT</u> CATCGAGCTTG AGCCCCCTCAAGCCCAAATTGTCGCCAATG	6469
15	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly23Term GGA-TGA	CATTGGCGACAAATTGGGCTT <u>GAGGGGGCTCAAGCTCGATGACC</u> CATTCCGAGCTTC <u>ACGGCCTAGAGGAGGTGTCGGGGACGGC</u> AGGGGGAAGAATGCAGAACTTGCAGCGGTGGC	6470
		CTAGGCCG <u>TGAAAGCTC</u>	6471
		GAGCTT <u>CACGGCCTAG</u>	6472
		ACCGCTGCAAGTTCTGCATTCTCCCCCTGCCGTCCCCGGACACC TCCTCTAGGCCGGG <u>ATAGCTCGGAAATGGGT</u> CATCGAGCTTGAGC CCCCTCAAGCCCAAATTGTCGCCAATGCCG	6473
		CGGCATTGGCGACAAATTGGGCTT <u>GAGGGGGCTCAAGCTCGAT</u> GACCCATTCCGAGCT <u>ATCCCGGCCTAGAGGAGGTGTCGGGGGA</u> CGGCAGGGGGAAAGAATGCAGAACTTGCAGCGGT	6474
20	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Lys24Term AAG-TAG	GGCCGGG <u>ATAGCTCGGA</u>	6475
		TCGGAGCT <u>ATCCCGGCC</u>	6476
		GCAAGTTCTGCATTCTCCCCCTGCCGTCCCCGGACACCCTCT AGGCCGGGAAAGCT <u>TGAAATGGGT</u> CATCGAGCTTGAGCCCCCT CAAGCCCAAATTGTCGCCAATGCCGGGTGA	6477
		TCAACCCGGCATTGGCGACAAATTGGGCTT <u>GAGGGGGCTCAAGC</u> TCGATGACCCATT <u>TCAGAGCTTCCGGCCTAGAGGAGGTGTCG</u> GGGACGGCAGGGGGAAAGAATGCAGAACTTGC	6478
25	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly26Term GGA-TGA		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAAAGCTC <u>T</u> GAAATGGG CCCATTT <u>C</u> AGAGCTTC	6479 6480
5 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Ser29Term TCA-TGA	CATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGAA AGCTCGGAAATGGGT <u>G</u> ATCGAGCTTGAGCCCCCTCAAGCCAAAT TTGTCGCCAATGCCGGTTGAAGGTTAAGGC GCCTTAACCTCAACCCGGCATTGGCGACAAATTGGGCTTGAGG GGGCTCAAGCTCGAT <u>C</u> ACCCATTCCGAGCTTCCGGCCTAGAG GAGGTGTCCGGGGACGGCAGGGGAAGAATG AAATGGGT <u>G</u> ATCGAGCT	6481 6482 6483 6484
10 Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Ser9Term TCG-TAG	CGTTTAAGTGGATGGACATTAAGTGTAAATCATGGTAGCTAT GAGTGCTACTGCGT <u>A</u> GCTGTTCCGGTTCTCCCAAAACCTCA CTCTGGAGCCAAGACATCTGATAAGCTTG CCAAGCTTATCAGATGTCTGGCTCCAGAGTGAGGTTGGGAA GAAACCGGAAACAGCTACGCAGTAGCACTCATAGCTACCATGATT AAAACACTAAATGTCGATCCACTAAACG TACTGCGT <u>A</u> GCTGTT GAAACAGCTACGCAGTA	6485 6486 6487 6488
15 Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys17Term AAA-TAA	AGTGTAAATCATGGTAGCTATGAGTGCTACTGCGTCGCTGTT CGGTTTCTCCCC <u>A</u> ACCTCACTCTGGAGCCAAGACATCTGATAA GCTTGGAGGTGAACCAGGTAGTGTGTT CAGCAACACTACCTGGTTCACCTCCAAGCTTATCAGATGTCTGGC TCCAGAGTGAGGT <u>A</u> TGGGAAGAAACCGGAAACAGCGACGCAG TAGCACTCATAGCTACCATGATTAACACT CTTCCCC <u>A</u> ACCTCAC GTGAGGTT <u>A</u> TGGGAAG	6489 6490 6491 6492
20 Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Gly21Term GGA-TGA	ATGGTAGCTATGAGTGCTACTGCGTCGCTGTTCCGGTTCTCCC CAAAACCTCACTCT <u>G</u> AGCCAAGACATCTGATAAGCTTGAGGTGA ACCAGGTAGTGTGCTGTGCGCGGAATCA TGATTCCCGCGCACAGCAACACTACCTGGTTCACCTCCAAGCTTATC AGATGTCTGGCT <u>A</u> AGAGTGAGGTTGGGAAGAAACCGGAAA CAGCGACCGCAGTAGCACTCATAGCTACCAT CTCACTCT <u>G</u> AGCCAAG CTTGGCT <u>A</u> AGAGTGAG	6493 6494 6495 6496

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys23Term AAG-TAG	GCTATGAGTGCTACTGCGTCGCTGTTCCGGTTCTCCCCAAAC CTCACTCTGGAGCC <u>T</u> AGACATCTGATAAGCTGGAGGTGAACCAG GTAGTGTGCTGTGCGCGGAATCAAGACAA	6497
		TTGTCTTGA <u>T</u> CCGCGCACAGCAACACTACCTGGTTCACCTCCAAG CTTATCAGATGT <u>T</u> AGGCTCCAGAGTGAGGTTGGGGAAAGAAC CGGAAACAGCGACGCAGTAGCACTCATAGC	6498
		CTGGAGC <u>T</u> AGACATCT	6499
		AGATGT <u>T</u> AGGCTCCAG	6500
10	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys21Term AAA-TAA	ATGGTGGCTGCTGCAGCAAGTCTGCATGCTTCCCTGTTCCATCC CCAGGAGCCTCCCT <u>T</u> AACCTGGGAAGTTAGGCAACTGGTCATCG AGTTTGAGCCCTCC <u>T</u> GAAGGCCAAGTCAA	6501
		TTGACTTGGGCTCAAGGAAGGGCTAAACTCGATGACCAGTTGC CTAACTTCCCAGGTT <u>A</u> AGGGAGGCTCTGGGATGGAACAGGG AAGCATGCAGAACTTGCTGCAGCAGCCACCAT	6502
		CCTCCCT <u>T</u> AACCTGGG	6503
		CCCAGGTT <u>A</u> AGGGAGG	6504
		GCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCCAGGAGCC TCCCCTAAACCTGGG <u>T</u> AGTTAGGCAACTGGTCATCGAGTTGAGC CCTTCC <u>T</u> GAAGGCCAAGTCAATCCCCAATG	6505
15	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys24Term AAG-TAG	CATTGGGGATTGACTTGGGCTCAAGGAAGGGCTAAACTCGATG ACCAGTTGC <u>T</u> AACT <u>AC</u> CCAGGTTAGGGAGGCTCTGGGATG GAACAGGGAAAGCATGCAGAACTTGCTGCAGC	6506
		AACCTGGG <u>T</u> AGTTAGGC	6507
		GCCTAACT <u>AC</u> CCAGGTT	6508
		TGCATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCTAAACCTGG GAAGTTAGGCAACTG <u>T</u> ATCGAGTTGAGCCCTCC <u>T</u> GAAGCC CAAGTC <u>A</u> ATCCCCAATGGCGGATT <u>T</u> CAGGTT	6509
20	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Trp28Term TGG-TGA	AACCTGA <u>A</u> ATCCGCCATTGGGATTGACTTGGGCTCAAGGAAGG GCTCAA <u>A</u> CTCG <u>T</u> GAT <u>G</u> ATCAGTTGC <u>T</u> AACTTCCCAGGTTAGGG GGCTCCTGGG <u>T</u> GAACAGGGAAAGCATGCA	6510
		GGCA <u>A</u> CTG <u>T</u> ATCGAG	6511
		CTCG <u>T</u> ATG <u>T</u> AGTTGCC	6512
		CATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCTAAACCTGG AGTTAGGCAACTGGG <u>T</u> ATCGAGTTGAGCCCTCC <u>T</u> GAAGCC AGTC <u>A</u> ATCCCCAATGGCGGATT <u>T</u> CAGGTTAA	6513
25	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Ser29Term TCA-TGA	TTAACCTGA <u>A</u> ATCCGCCATTGGGATTGACTTGGGCTCAAGGAA GGGCTCAA <u>A</u> CTCG <u>T</u> GAT <u>C</u> ACCAGTTGC <u>T</u> AACTTCCCAGGTTAGGG GAGGCTCCTGGG <u>T</u> GAACAGGGAAAGCATG	6514

Phenotype: Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys21Term AAA-TAA	CAACTGGT <u>G</u> ATCGAGTT	6515
	AACTCGAT <u>C</u> ACCAGTTG	6516
	ATGGTGGCTGCCGAGCAAGTCTGCATTCTCCGTTCCAACC CCGGGAATCTCCCCT <u>T</u> AACCCGGGAAGTCGGTAATGGTGGCTT CAGGTTAAGGCAAACGCCAATGCCCATCCTA	6517
	TAGGATGGGCATTGGCGTTGCCTAACCTGAAAGGCCACCATTAC CGAACTTCCC <u>G</u> GGTT <u>A</u> AGGGGAGATTCCC <u>G</u> GGTTGGAACGGAG AAGAATGCAGAACTTGCTGCCGCAGCCACCAT	6518
	TCTCCC <u>T</u> TAACCCGGG	6519
10 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG	CCCGGG <u>T</u> TAAGGGGAGA	6520
	GCCGCAGCAAGTTCTGCATTCTCCGTTCCAACCCGGGAATC TCCCCTAAACCCGGG <u>T</u> AGTTCGGTAA <u>T</u> GGTGGCTT <u>C</u> AGGTTAAG GCAAACGCCAATGCCCATCCTAGTCTAAAGT	6521
	ACTTTAGACTAGGATGGGCATTGGCGTTGCCTAACCTGAAAGCC ACCATTACCGAA <u>T</u> ACCCGGGTTAGGGGAGATTCCC <u>G</u> GGTTGG AACGGAGAAGAAC <u>T</u> GCAGAA <u>T</u> TGCTGCCGC	6522
	AACCCGGG <u>T</u> AGTT <u>C</u> GGT	6523
	ACCGAA <u>T</u> ACCCGGGTT	6524
15 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gln31Term CAG-TAG	TTCTCCGTTCCAACCCCGGGAA <u>T</u> CTCCC <u>T</u> AAACCCGGGAAG <u>T</u> TC GGTAATGGTGGCTT <u>T</u> AGGTTAAGGCAAACGCCAATGCCCATCCT AGTCTAAAGTCTGGCAGCCTCGAGACTGAAG	6525
	CTTCAGTCTCGAGGC <u>T</u> GCCAGACT <u>T</u> AGACTAGGATGGCATTGG CGTTTGCC <u>T</u> TAAC <u>T</u> AAAGCCACCATTACCGAA <u>T</u> CC <u>G</u> GGTT AGGGGAGATTCCC <u>G</u> GGTTGGAACGGAGAA	6526
	GTGG <u>T</u> TT <u>T</u> AGGTTAAG	6527
	CTTAAC <u>T</u> AAAGCCAC	6528
	GTTCCAACCCCGGGAA <u>T</u> CTCCC <u>T</u> AAACCCGGGAAG <u>T</u> TCGGTAAT GGTGGCTT <u>C</u> AGGTT <u>T</u> AGGCAAACGCCAATGCCCATCCTAGTCTA AAGTCTGGCAGCCTCGAGACTGAAGATGACA	6529
20 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys33Term AAG-TAG	TGT <u>C</u> AT <u>T</u> TCAGTCTCGAGGC <u>T</u> CCAGACT <u>T</u> AGACTAGGATGGG CATTGG <u>C</u> TTGC <u>T</u> AAAC <u>T</u> CTGAAAGCCACCATTACCGAA <u>T</u> CC <u>G</u> GGGTTAGGGGAGATTCCC <u>G</u> GGTTGGAAC	6530
	TTCAGG <u>T</u> TT <u>T</u> AGGCAAAC	6531
	GTTTG <u>C</u> CTAAAC <u>T</u> CTGAA	6532

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Gln21Term CAA-TAA	ATGTTGAAGCTCTCGTGTATGCGACTGATAAGTTACAGACCCCTCTCTCGCATTCTCATTAACCGGATCCGGCACACCCGGAGAACCGTCTCCTCGGTGTGCTCTCATCTGAGGAAC	6533
		GTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGTGTGCTCTCATCTGAGGAAC	6534
		TATCAGTCGCATTACACGAGAGCTTCAACAT	6535
		ATTCTCATTAACCGGAT	6536
10	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Arg28Term AGA-TGA	GCGACTGATAAGTTACAGACCCCTTTCTCGCATTCTCATCAACCGGATCCGGCACACCCGGTGAACCGTCTCCTCCGTGTGCTCTCATC	6537
		TGAGGAAACCGGTTCTCGATCCTTGCAG	6538
		CTCGCAAAGGATCGAGAACCGGTTCTCAGATGAGAGCACGACA	6539
		CGGAGGAGACGGTCAACCGGTGTGCCGGATCCGGTTGATGAGAA	6540
		TGCGAGAAGAGGGCTGTAACTTATCAGTCGC	
15	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Ser24Term TCG-TAG	CACACCGGTGAACCGTC	6541
		GACGGTTCAACCGGTGTG	6542
		CCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCCGGAGAA	6543
		CCGTCTCCTCCGTGTAGTGTCTCATCTGAGGAAACCGGTTCTCG	6544
		ATCCTTGCAGCGATCGTATCTGCTGATCA	
20	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Cys25Term TGC-TGA	TGATCAGCAGATACGATCGCTCGAAAGGATCGAGAACCGGTTTC	6545
		CTCAGATGAGAGCACTACACGGAGGAGACGGTTCTCCGGTG	6546
		CGGATCCGGTTGATGAGAACGAGAGGG	6547
		CTCCGTGTAGTGTCTC	6548
		GAGAGCACTACACGGAG	
25	Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Leu2Term TTG-TAG	CTTCTCGCATTCTCATCAACCGGATCCGGCACACCCGGAGAACCGT	6549
		CTCCCTCGTGTGATCTCATCTGAGGAAACCGGTTCTCGATCC	6550
		TTTGCAGCGATCGTATCTGCTGATCAAGGA	
		TCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGG	
		TTTCCTCAGATGAGATCACGACACGGAGGAGACGGTTCTCCGGTG	
		TGCCGGATCCGGTTGATGAGAACGAGAG	
		GTGTCGTGATCTCATCT	
		AGATGAGATCACGACAC	
		ATTCCTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAGG	
		GCATCAAAATGTAGAAGCTTCGTGTATGTGACTAACAACTTAC	
		ACACCTTCTCCTTCTCCGATTCCTC	
		GAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTAGTCACA	
		TTACACGAAAGCTTACATTGATGCCCTTTTTTTATGGTC	
		CTGAGGTTGGTTATAGAAGAAGAAT	

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAATGT <u>A</u> GAAGCTTT	6551
	AAAGCTT <u>C</u> TACATTTT	6552
5 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Lys3Term AAG-TAG	TCTTCTTCTATAACCAAAACCTCAGGAACCATAAAAAAAAAGGG CATCAAAATGTT <u>G</u> AGCTTCGTGAATGTGACTAACAACTTACAC ACCTTCTCCTCTCTCCGATTCCCTCCC	6553
	GGGAGGAATCGGAGAAGAAGGAGAAGGTGTGAAGTTGTTAGTCA CATTACACGAAAGCT <u>A</u> CAACATTGGATGCCCTTTTTATGG	6554
	TTCCGTAGGTTGGTTATAGAAGAAGA	
	AAATGTT <u>G</u> AGCTTCG	6555
	CGAAAGCT <u>A</u> CAACATT	6556
10 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Ser5Term TCG-TAG	CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAGGGCATCAA AATGTTGAAGCTT <u>A</u> GTGAATGTGACTAACAACTTACACACCTCT CCTCTTCTCCGATTCCCTCCCTTTCAT	6557
	ATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGAAGTTG TTAGTCACATTACACT <u>A</u> AGCTCAACATTGGATGCCCTTTTT	6558
	TTATGGTTCCCTGAGGTTGGTTATAG	
	GAAGCTT <u>A</u> GTGAATG	6559
	CATTACACT <u>A</u> AGCTTC	6560
15 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Cys6Term TGT-TGA	AAACCAAAACCTCAGGAACCATAAAAAAAAAGGGCATAAAAATG TTGAAGCTTCGTGA <u>A</u> ATGTGACTAACAACTTACACACCTCTCCT CTTCTCCGATTCCCTCCCTTTCATCCCG	6561
	CGGGATGAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGA AGTTGTTAGTCACATT <u>C</u> ACGAAAGCTCAACATTGGATGCCCTT	6562
	TTTTTTATGGTTCCCTGAGGTTGGTT	
	CTTCGT <u>G</u> AAATGTGAC	6563
	GTCACATT <u>C</u> ACGAAAG	6564

**Table 23**  
**Oligonucleotides to produce plants with increased stearate**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Lys4Term AAG-TAG	GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGATTCAATTATCATATC CAGAAATGGCTCTATAGTTAACCTTGGTGGCATCTCAGCCTTA CAAATCCCTTCCTCGACTCGTCCGCCAA	6565
		TTGGCGGACGAGTCGAGGAAGGGATTGTAGGCTGAGATGCCA CCAAAGGGTAAACTATAGAGCCATTCTGGATATGATGAATGAAT CCTCTTTCTACAGAGCTAGAGCTCTCCC	6566
		TGGCTCTATAGTTAAC	6567
		GTTAAACTATAGAGCCA	6568
10	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Leu8Term TTG-TAG	CTCTGTAGAAAAGAAGGATTCAATTATCCAGAAATGGCTCT AAAGTTAACCTT <del>AG</del> GTGGCATCTCAGCCTTACAAATTCCCTTCC TCGACTCGTCCGCCAACTCCTTCTTCAG	6569
		CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGATTGTAA GGCTGAGATGCCACCTAAGGGTAAACTTAGAGCCATTCTGGAT ATGATGAATGAATCCTCTTCTACAGAG	6570
		TAACCCTT <del>AG</del> GTGGCAT	6571
		ATGCCACCTAAGGGTTA	6572
		AGAAGGATTCAATTATCCAGAAATGGCTCTAAAGTTAAC CTTGGTGGCATCT <del>T</del> AGCCTTACAAATTCCCTCCTCGACTCGTCC GCCAACTCCTCTTCAAGATCTCCCAAGT	6573
15	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Gln12Term CAG-TAG	ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAA GGGAATTGTAGGCTAAGATGCCACCAAGGGTAAACTTAGAG CCATTCTGGATATGATGAATGAATCCTTCT	6574
		TGGCATCT <del>T</del> AGCCTTAC	6575
		GTAAGGCTAAGATGCCA	6576
		TCATTCAATCCAGAAATGGCTCTAAAGTTAACCTTGGTG GCATCTCAGCCTT <del>A</del> AAATTCCCTCCTCGACTCGTCCGCCAACTC CTTCTTCAGATCTCCCAAGTCTCTGC	6577
20	Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Phe14Term TAC-TAG	GCAGAGGAACCTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAG TCGAGGAAGGGATTCTAAGGCTGAGATGCCACCAAGGGTAA ACTTCTAGAGCCATTCTGGATATGATGAATGA	6578
		CAGCCTT <del>A</del> AAATTCCC	6579
		GGGAATTCTAAGGCTG	6580

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu3Term TTG-TAG	GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAA AAAGAAAATGGCATAGAACGTTAACCCTTGGCATCTCAGCCTTAC AAACTCCCTCCTCGGCTCGTCCGCCAAT	6581
		ATTGGCGGACGAGCCGAGGAAGGGAGTTGTAAGGCTGAGATGC CAAAGGGTTAACGCTCTATGCCATTTCAGACACGAGCGAGCTCTC	6582
		AATGGCATAAGCTTA	6583
		TAAGCTTCTATGCCATT	6584
10	Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Lys4Term AAG-TAG	GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAAA AGAAAATGGCATTTGCTAACCCCTTGGCATCTCAGCCTTACAA ACTCCCTCCTCGGCTCGTCCGCCAATCT	6585
		AGATTGGCGGACGAGCCGAGGAAGGGAGTTGTAAGGCTGAGAT GCCAAAGGGTTAACGCTAACATGCCATTTCAGACACGAGCGAGCTC	6586
		TGGCATTGTAAGCTTAAC	6587
		GTAAAGCTAACATGCCA	6588
		TCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATT GAAGCTAACCCCTAGGCATCTCAGCCTAACAAACTCCCTCCTCG GCTCGTCCGCCAATCTACTCTCAGATC	6589
15	Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu8Term TTG-TAG	GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTT GTAAGGCTGAGATGCCAACGGTTAACGCTTCAATGCCATTTCAGA	6590
		TAACCCTTAGGCATCTC	6591
		GAGATGCCAACGGTTA	6592
		AACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATTGAAGCTTAA CCCTTGGCATCTTACGCTTACAAACTCCCTCCTCGGCTCGTCCG CCAATCTACTCTCAGATCTCCAAGT	6593
20	Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Gln11Term CAG-TAG	ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAA GGGAGTTGTAAGGCTAACGATGCCAACGGTTAACGCTTCAATGCC ATTTCTTTTGTACGAGGTTGATGTT	6594
		TGGCATCTTACGCTTAC	6595
		GTAAGGCTAACGATGCCA	6596
		AACCAAAAGAAAAGGTAAAGAAAAAAACAATGGCTCTCAAGCTCA ATCCTTCCCTTCTAACCCAAAAGTTACCTTCTTCGCTCTCCA CCAATGGCCAGTACCAAGATCTCTAACGTT	6597
25	Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln27Term CAA-TAA	ACTTAGGAGATCTGGTACTGGCATTGGTGGAAAGAGCGAAAGAAG GTAACCTTGGTTAACGAAAGGAAAGGATTGAGCTTGAGAGCCAT	6598
		TGTTTTTCTTACCTTTCTTGGTT	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln29Term CAA-TAA	TCCTTTCT <u>TAAACCCAA</u>	6599
		TTGGGTT <u>AAGAAAGGA</u>	6600
		AAGAAAAAGGTAAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTT TCCTTTCTCAAACCTAAAGTTACCTCTTCGCTCTCCACCAATG GCCAGTACCAAGATCTCTAAAGTTCTACA	6601
		TGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGAAGAGCGA AAGAAGGTAACT <u>TTTAGGTTGAGAAAGGAAAGGATTGAGCTTGAG</u> AGCCATTGTTTTTTCTTACCTTTCTT	6602
		CTCAAAC <u>CTAAAAGTTA</u>	6603
		TAACTTT <u>AGGTTTGAG</u>	6604
	Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys30Term AAG-TAG	AAAAAGGTAAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTCC TTTCTCAAACCC <u>AAATAGTTACCTCTTCGCTCTCCACCAATGGC</u> CAGTACCAAGATCTCTAAAGTTCTACATGG	6605
		CCATGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGAAGAG CGAAAGAAGGTAACT <u>ATTGGGTTGAGAAAGGAAAGGATTGAGCT</u> TGAGAGCCATTGTTTTTTCTTACCTTTT	6606
		AAACCC <u>AAATAGTTACCT</u>	6607
		AGGTAACT <u>ATTGGGTTT</u>	6608
		TCTCAAACCCAAAAGTTACCTCTTCGCTCTCCACCAATGCCA GTACCAGATCTCCT <u>TTAGTTCTACATGGCCTCTACCCCTCAAGTCTGG</u> TTCTAAGGAAGTTGAGAATCTCAAGAAGC	6609
15	Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys46Term AAG-TAG	GCTCTTGAGATTCTCAACTCTCTAGAACCAAGACTTGAGGGTAGA GGCCATGTAGAACT <u>AAGGAGATCTGGTACTGGCATTGGTGAAG</u> AGCGAAAGAAGGTAACTTTGGGTTGAGA	6610
		GATCTCCT <u>TTAGTTCTAC</u>	6611
		GTAGAACT <u>AAGGAGATC</u>	6612
		TCTTCTGATTCA <u>TTAATCTTACTCATCAATGGCTCTGAGACTGAA</u> CCCTATCCCCAC <u>CTAAACCTTCCCTCCCCAAATGCCAGTCT</u> CAGATCTCCCAGGTTCCGCATGCCCTCTA	6613
		TAGAGGCCATGCCAACCTGGGAGATCTGAGACTGCCATTGG GGGAGGGAGAAGGTT <u>TTAGGTGGGATAGGGTTCAGTCTCAGAGC</u> CATTGATGAGTAAAGATTAAATGAATCAGAAGA	6614
20	Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln11Term CAA-TAA	TCCCCAC <u>CTAAACCTTC</u>	6615
		GAAGGTT <u>TTAGGTGGGAA</u>	6616

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligo	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln17Term CAA-TAA	CTTTACTCATCAATGGCTCTGAGACTGAACCCATCCCCACCCAAA CCTCTCCCTCCCCAAATGGCCAGTCTCAGATCTCCAGGTTCC GCATGGCCTCTACCCCTCGCTCCGGTTCCA	6617
		TGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGAT CTGAGACTGGCCATTAGGGGAGGGAGAAGGTTGGTGGGAT AGGGTTCACTCTCAGAGCCATTGATGAGTAAAG	6618
		CCCTCCCCAAATGGCC	6619
		GGCCATTAGGGAGGG	6620
10	Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Arg22Term AGA-TGA	GCTCTGAGACTGAACCCATCCCCACCCAAACCTTCTCCCTCCCC CAAATGGCCAGTCTCTGATCTCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCCAAGAGAGGTTGAAAATA	6621
		TATTTCAACCTTTGGAACCGGAGCGGAGGGTAGAGGCCATGC GGAACCTGGGAGATCAGAGACTGGCCATTGGGGGAGGGAGAAG GTTGGGTGGGGATAGGGTTCACTCTCAGAGC	6622
		CCAGTCTCTGATCTCCC	6623
		GGGAGATCAGAGACTGG	6624
		CAAATGGCCAGTCTCAGATCTCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCTAACAGAGGTTGAAAATATTAAGAACCCATTCA CTCCTCCCAGAGAAGTGCATGTTCAAGTAA	6625
15	Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Lys37Term AAA-TAA	TTACTGAACATGCACTCTCTGGGAGGAGTGAATGGCTCTTAAT ATTTCAACCTCTTAGGAACCGGAGCGGAGGGTAGAGGCCATGCG GAACCTGGGAGATGTGAGACTGGCCATTG	6626
		CCGGTTCTAACAGAGGTT	6627
		AACCTCTTAGGAACCGG	6628
		CAACAAAGCACACACAAGAACACATCAACAAATGGCGATTGCATCA ATACGGCGACGTTTAATCAGACCTGTACCGTTATTGCCTTCC TCAACCGAAACCTCTCAGATCTCCCAAAT	6629
		ATTTGGGAGATCTGAGAGGTTGGTTGAGGAACCGCGAATGAAC GGTACAGGTCTGATTAACACGTGCCGTATTGATGCGAATGCCA TTGTTGATGTTCTGTGTGCTTGTGTTG	6630
20	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA	CGACGTTTAATCAGAC	6631
		GTCTGATTAACACGTG	6632
		AAGCACACACAAGAACACATCAACAAATGGCGATTGCATCAATAC GGCGACGTTCAATGAGACCTGTACCGTTATTGCCTTCCCAA	6633
		CCGAAACCTCTCAGATCTCCCAAATTCGC	
		GCGAATTGGGAGATCTGAGAGGTTGGTTGAGGAACCGCGAAT GAACGGTACAGGTCTATTGAAACGTGCCGTATTGATGCGAATC	6634
30	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser12Term TCA-TGA	GCCATTGTTGATGTTGTTCTGTGTGCTT	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAC-TAG	GTTTCAAT <u>GAGACCTGT</u>	6635
		ACAGGTCT <u>ATTGAAAC</u>	6636
		AAGAACAA <u>CATCAACAATGGCGATTCGCATCAATACGGCGACGTT</u> CAATCAGAC <u>CTGTAGCGTCATT</u> TCAGAT <u>CTCCCAAATTGCCATGGCTTC</u>	6637
		GGAAGCC <u>CATGGCGAATTGGGAGATCTGAGAGGTT</u> TGAGGAAAC <u>CGCAATCAACGGTACAGGCTGATTGAAACGTCGCCGTATT</u> GAT <u>CGAATGCCATTGTTGATGTTGTTCTT</u>	6638
		GAC <u>CTGTAGCGTT</u> CATT	6639
		AAT <u>GAACGCTACAGGTC</u>	6640
10	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser17Term TCA-TGA	CAACAT <u>CAACAATGGCGATTCGCATCAATACGGCGACGTTCAATC</u> AGAC <u>CTGTACCGTTGATT</u> TC <u>CGCGTTCTCAACCGAAACCTCTCAGA</u> TCT <u>CCCAAATTGCCATGGCTTCACCAT</u>	6641
		ATGGT <u>GGAAAGCCATGGCGAATTGGGAGATCTGAGAGGTT</u> TGAGGAAAC <u>CGCAATCAACGGTACAGGCTGATTGAAACGTCGCC</u> GTATTGAT <u>CGAATGCCATTGTTGATGTTG</u>	6642
		GT <u>ACCGTTGATT</u> CGCGT	6643
		AC <u>CGCGAATCAACGGTAC</u>	6644
		ACAC <u>ACACACACACTCAATCACACACACATCATCATCTTCTTCATC</u> AAC <u>CGATGGCGCTT</u> AT <u>ATCCTTCATACACTTTCATCAATCGA</u>	6645
15	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Arg4Term CGA-TGA	TCGATTGAT <u>AAAAGTGTATGAGGATAT</u> AT <u>CTCCCGTTGAAGCGT</u> CAC <u>CGGACTCATTCAAAAGGCCATCGTTGATGAAAGAAGATGATGA</u> TGT <u>GTGTGATTGAGTGTGTGTGT</u>	6646
		TGGCG <u>CTT</u> GAAT <u>GAGT</u>	6647
		ACT <u>CATTCAAAAGGCCA</u>	6648
		ACACACACAT <u>CATCATCTTCTTCATCAACGATGGCGCTTCGAATGA</u> GT <u>CCGGTGACGCTT</u> TCA <u>ATCGAAAATCTCAGATCTCCTAAAT</u>	6649
		AT <u>TTAGGAGATCTGAGATTTTCGATTGATGAAAGTGTATGAAGG</u> AT <u>ATATCTCCCGTT</u> AA <u>AGCGTCACCGGACTCATTGAAAGCGCCAT</u> CG <u>TTGATGAAAGAAGATGATGATGTTGTGT</u>	6650
20	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA	TGACG <u>CTT</u> AAC <u>GGGAG</u>	6651
		CT <u>CCCGTT</u> AA <u>AGCGTCA</u>	6652

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Glu13Term GAG-TAG	ACATCATCATCTTCTTCATCAACGATGGCGCTCGAATGAGTCGG TGACGCTTCAACGGTAGATATCCTTCATACACTTTCATCAATCG AAAAATCTCAGATCTCCTAAATTGCGGA	6653
		TCGCGAATTAGGAGATCTGAGATTTTCGATTGATGAAAAGTGT TGAAGGATATATCT <u>ACCGTTGAAGCGTCACCGGACTCATTGAA</u> CGCCATCGTTGATGAAGAAGATGATGATGT	6654
		TTCAACGGTAGATATAT	6655
		ATATATCT <u>ACCGTTGAA</u>	6656
10	Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAT-TAG	ATCTTCTTCATCAACGATGGCGCTCGAATGAGTCGGTGACGCTT CAACGGGAGATATA <u>G</u> CTTCATACACTTTCATCAATCGAAAATCT CAGATCTCCTAAATTGCGATGGCTTCC	6657
		GGAAGCCATCGCAATTAGGAGATCTGAGATTTTCGATTGATGA AAAGTGTATGAAGG <u>C</u> TATATCTCCCGTTGAAGCGTCACCGGACTC ATTGAAGCGCCATCGTTGATGAAGAAGAT	6658
		GAGATATA <u>G</u> CTTCATA	6659
		TATGAAGG <u>C</u> TATATCTC	6660
		AACTCAGCCAGCTGCCCCAAACAACAGCGCAGAAAAACCTTCA ACAACAATGGCTCT <u>C</u> TAGCTCAACCCAGTCACCACCTCCCTCAA CACGCTCCCTCAACA <u>ACTT</u> CTCCTCCAGAT	6661
15	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys4Term AAG-TAG	ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTGAAGGGAAAGGTG GTGACTGGGTTGAG <u>C</u> TAGAGAGCCATTGTTGTTGAAGGTTTCTG CGCTGTTTTGGGGCAAGCTGGCTGAGTT	6662
		TGGCTCT <u>C</u> TAGCTAAC	6663
		GTTGAG <u>C</u> TAGAGAGCC	6664
		GGCGAGAAAAACCTCAACAACAATGGCTCTCAAGCTCAACCCAG TCACCACCTCCCTT <u>G</u> AACACGCTCCCTCAACA <u>ACTT</u> CTCCTCCAG ATCTCCTCGCAC <u>CTT</u> CTCATGGCTGCTT	6665
20	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Ser13Term TCA-TGA	GAAGCAGCCATGAGAAAGGTGCGAGGAGATCTGGAGGAGAAGTT GTTGAGGGAGCGTGT <u>C</u> AAGGGAAAGGTGGTACTGGGTTGAGCT TGAGAGCCATTGTTGTTGAAGGTTTCTGCGC	6666
		CTTCCCTT <u>G</u> AACACGCT	6667
		AGCGTGT <u>C</u> AAGGGAAAG	6668
		CTCAAGCTCAACCCAGTCACCACCTCCCTCAACACGCTCCCTC AACAA <u>CTT</u> CTCCTCCT <u>G</u> ATCTCCTCGCAC <u>CTT</u> CTCATGGCTGCTT CCACTTCAATTCCACCTCCACCAAGTAAG	6669
25	Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Arg23Term AGA-TGA	CTTACTTGGTGGAGGTGGAATTGAAAGTGGAAAGCAGCCATGAGAA AGGTGCGAGGGAGAT <u>C</u> AGGAGGAGAAGTTGTTGAGGGAGCGTGT	6670
		GAAGGGAAAGTGGTACTGGGTTGAGCTTGAG	
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys41Term AAG-TAG	TCTCCTCCT <u>T</u> GATCTCCT	6671
	AGGAGATCAGGAGGAGA	6672
	TCCTCCAGATCTCCTCGCACCTTCTCATGGCTGCTTCCACTTCA ATTCCACCTCCACCT <u>T</u> GTAAGCATCTCCTCCTCGGAATCTCCG CCGATTTC <u>T</u> TAAGCGATTGATCGTAGA	6673
	TCTACGATCAATCGCTAAAAGAAATCGGGGAGATTCCGAGGAG GAGGAGATGCTTACT <u>A</u> GGTGGAGGTGGAATTGAAAGTGGAAAGCAG CCATGAGAAAGGTGCGAGGAGATCTGGAGGA	6674
	CCTCCACCT <u>A</u> GTAAAGCA	6675
	TGCTTACT <u>A</u> GGTGGAGG	6676
	ATGGCACTGAAACTTTGCTTTCAACCCACAAGATGCCTCCCTCC CCGATGCTCGTAT <u>T</u> GATCTCACAGGGTTTCATGGCTTCAACTAT TCATTCTCCTCTATGGAGGTGGAAAAG	6677
	CTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAA AACCTGTGAGAT <u>C</u> AGATACGAGCATGGGAAGGAAGGCATCTT GTGGGGTGGAAAGCAAAGTTCAAGTGCCAT	6678
	CTCGTAT <u>T</u> GATCTCAC	6679
	GTGAGAT <u>C</u> AGATACGAG	6680
10 Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Arg21Term AGA-TGA	CCCACAAGATGCCTCCCTCCCCGATGCTCGTATCAGATCTCAC GGGTTTCATGGCTT <u>G</u> AACTATTCAATTCTCCTCTATGGAGGTGG AAAAGTTAAAAGCCTTCACGCCCTCCACG	6681
	CGTGGAGGCGTGAAGGTTAACTTTCCGACCTCCATAGAAG GAGAATGAATAGTTCAAGCCATGAAACCCCTGTGAGATCTGATACG AGCATGGGGAGGAAGGCATCTGTGGG	6682
	CATGGCTT <u>G</u> AACTATT	6683
	GAATAGTT <u>C</u> AAGCCATG	6684
	GATGCTCGTATCAGATCTCACAGGGTTTCATGGCTTCAACTATT ATTCTCCTCTATG <u>T</u> AGGTGGAAAAGTTAAAAGCCTTCACGCC TCCACGAGAGGTACATGTTCAAGTAACCC	6685
15 Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Ser29Term TCA-TGA	GGGTTACTGAACATGTACCTCTCGTGGAGGC <u>G</u> TGAAAGGCTTT AACTTTCCGACCT <u>A</u> CATAGAAGGAGAATGAATAGTTGAAGCCATG AAAACCC <u>T</u> GTGAGATCTGATACGAGCATC	6686
	CTTCTATG <u>T</u> AGGTGGGA	6687
	TCCGACCT <u>A</u> CATAGAAG	6688

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Gly39Term GGA-TGA	CGTATCAGATCTCACAGGGTTTCATGGCTCACTATTCAATTCTC CTTCTATGGAGGTCT <u>GAAAAGTTAAAAGCCTTCACGCCTCCACG</u> AGAGGTACATGTTCAAGTAACCCATTCTC	6689
		AGGAATGGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAG GCTTTTA <u>ACTTTCA</u> GACCTCCATAGAAGGAGAATGAATAGTTGA AGCCATGAAAACCTGTGAGATCTGATACG	6690
		TGGAGGTCT <u>GAAAAGTT</u>	6691
		AACTTT <u>CA</u> GACCTCCA	6692
10	Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys4Term AAA-TAA	TTCTCGTTTGTCTGCCCCCTCTGCTCTCTCTATCAGGCACG GAGAAATGGCACT <u>GTA</u> ACTCAGTCCAGTCATGTTCAATCTCAGAA GCTCCATTCTGCTCCTATCCGCCTT	6693
		AAGGCGGATAGGAGGCAAGAAATGGAAGCTCTGAGATTGAAACA TGACTGGACTGAGTT <u>ACAGTGCCATTCTCCGTGCCTGATAGAGA</u> GAGAGAGCAGAGGGGACGACAAAAACGAGAA	6694
		TGGCACT <u>GTA</u> ACTCAGT	6695
		ACTGAGTT <u>ACAGTGCCA</u>	6696
15	Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln11Term CAA-TAA	CTGCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTC AGTCCAGTCATGTT <u>TAATCTCAGAAGCTCCATTCTGCCTCCTA</u> TCCGCCTTCCAATCTCAGATCTCCGAGGG	6697
		CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAAT GGAAGCTCTGAGATT <u>AAAACATGACTGGACTGAGTTCACTGCCA</u> TTTCTCCGTGCCTGATAGAGAGAGAGCAG	6698
		TCATGTT <u>TAATCTCAG</u>	6699
		CTGAGATT <u>AAAACATGA</u>	6700
20	Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln13Term CAG-TAG	TCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCA GTCATGTT <u>CAATCT</u> <u>TAGAAGCTCCATTCTGCCTCCTATCCGC</u> CTTCAATCTCAGATCTCCGAGGGTTTC	6701
		TGAAAACCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAA GAAATGGAAGCT <u>TAAGATTGAAACATGACTGGACTGAGTTCA</u> TGCCATTCTCCGTGCCTGATAGAGAGAGA	6702
		TTCAATCT <u>TAGAAGCTT</u>	6703
		AAGCTT <u>CTAAGATTGAA</u>	6704
25	Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys14Term AAG-TAG	CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTC ATGTT <u>CAATCTCAGT</u> <u>AGCTTCCATTCTGCCTCCTATCCGCCTC</u> CAATCTCAGATCTCCGAGGGTTTCATGG	6705
		CCATGAAAACCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGG CAAGAAATGGAAG <u>CTACTGAGATTGAAACATGACTGGACTGAGTT</u> CAGTGCCATTCTCCGTGCCTGATAGAGAG	6706
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Tyr12Term TAC-TAG	AATCTCAG <u>T</u> AGCTTCCA	6707
		TGGAAG <u>C</u> T <u>A</u> CTGAGATT	6708
		CCCCGAGATCTCGCTGCCGCTGCTATGGCGTCGCCGCGTCCC ACACCGCATGCCGT <u>A</u> GT <u>C</u> CTGCCGGCGTGGCGCAGAGGAG GAGCAATGGGATGT <u>C</u> GAAGATGGTGGCCATGGCC	6709
		GGCCATGGCCACC <u>A</u> CTTCGACAT <u>CC</u> ATTGCTCCTCTGC <u>G</u> CACGCCGCCGCAGG <u>A</u> CTACGGCGATGCCGTGGGACGCCCG AACGCCATGAGCAGCGGCAGCGAGATCTGGGG	6710
		TCGCCGT <u>A</u> GT <u>C</u> CTGCCGG	6711
		CCGCAGG <u>A</u> CTACGGCGA	6712
	Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Gln19Term CAG-TAG	CTGCTCATGGCITGCCGCCGTCCCACACCGCATGCCGTACTC CTGCCGCCGTGGCG <u>T</u> AGAGGAGGAGCAATGGGATGT <u>C</u> GAAGA TGGTGGCCATGCCCTCCACC <u>A</u> CACAGGGTCA	6713
		TGACCTGTTGATGGTGGAGGCCATGCCACC <u>A</u> CTTCGACATCC CATTGCTCCTCT <u>C</u> ACGCCACGCCGCCAGGAGTACGGCGAT GCCGTGTGGGACGCCCGAACGCCATGAGCAG	6714
		GCGTGGCG <u>T</u> AGAGGAGG	6715
		CCTCCT <u>C</u> ACGCCACGC	6716
		CCCACACCGCATGCCGTACTCCTGCCGCCGTGGCGCAGAG GAGGAGCAATGGGATGT <u>A</u> GAAGATGGTGGCCATGCCCTCCACCA TCAACAGGGTCAAGACTGCTAAGAAGCCCTACAC	6717
15	Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Ser26Term TCG-TAG	GTGTAGGGCTTCTAGCAGTCTGACCCTGTTGATGGTGGAGGCC ATGCCACC <u>A</u> CTCT <u>C</u> AC <u>AT</u> CCATTGCTCCTCTGCCACG CCGCCGCCAGGAGTACGGCGATGCCGTGGGG	6718
		TGGGATGT <u>A</u> GAAGATGG	6719
		CCATCTT <u>C</u> AC <u>AT</u> CCCA	6720
		CACACCGCATGCCGTACTCCTGCCGCCGTGGCGCAGAGGAG GAGCAATGGGATGT <u>C</u> GTAGATGGTGGCCATGCCCTCCACCA CAGGGTCAAGACTGCTAAGAAGCCCTACACTC	6721
		GAGTGTAGGGCTTCTAGCAGTCTGACCCTGTTGATGGTGGAGG CCATGCCACC <u>A</u> CT <u>C</u> AC <u>AT</u> CCATTGCTCCTCTGCCCA GCCGCCGCCAGGAGTACGGCGATGCCGTGTG	6722
20	Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Lys27Term AAG-TAG	GGATGTCGT <u>A</u> GTGGTG	6723
		CACCAT <u>C</u> AC <u>GT</u> ACATCC	6724

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Leu3Term TTG-TAG	TTCTCTCTAGGTGAGCGGTACCAACAGAACCTAGGAGA GAGAAGCAATGGCGT <del>A</del> GAAGCTTACCCACCGCCTCAATCCTT CCATGGCGGTACCTCTCGGGACTTCCTCG	6725
		CGAGGAAGTCCCAGAGAGGTAAACGCCATGGAAGGATTGAAGC CGTGTGGTGAAGCTT <del>C</del> ACGCCATTGCTCTCTCCTAAGTGCTT CTGTTGGTAACCGCTAACCTAGAGAGAGAA	6726
		AATGGCGT <del>A</del> GAAGCTTC	6727
		GAAGCTT <del>C</del> ACGCCATT	6728
		CTCTCTCTAGGTGAGCGGTACCAACAGAACCTAGGAGAGA GAAGCAATGGCGTTGAGCTTACCCACCGCCTCAATCCTCC ATGGCGGTACCTCTCGGGACTTCCTCGAT	6729
10	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Lys4Term AAG-TAG	ATCGAGGAAGTCCCAGAGAGGTAAACGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCT <del>A</del> CAACGCCATTGCTCTCTCCTAAGTG CTTCTGTTGGTAACCGCTAACCTAGAGAGAG	6730
		TGGCGTTG <del>T</del> AGCTTCAC	6731
		GTGAAGCT <del>A</del> CACGCCA	6732
		AAGCAATGGCGTTGAGCTTACCCACCGCCTCAATCCTCCAT GGCGGTACCTCT <del>A</del> GGGACTTCCTCGATCGTATCACCTCAGATC TCACCGCGTTTCATGGCTCTTACAAT	6733
		ATTGTAGAAGAACCATGAAAACCGCGGTGAGATCTGAGGTGATAC GATCGAGGAAGTCC <del>T</del> AAAGAGGTAAACGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTTCAACGCCATTGCTT	6734
15	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Ser19Term TCG-TAG	TACCTCT <del>A</del> GGGACTTC	6735
		GAAGTCC <del>T</del> AAAGAGGTAA	6736
		GCAATGGCGTTGAGCTTACCCACCGCCTCAATCCTCCATG GCGGTACCTCTCG <del>T</del> GACTTCCTCGATCGTATCACCTCAGATCTC	6737
		ACCGCGTTTCATGGCTTCTTACAATTG CAATTGTAGAAGAACCATGAAAACCGCGGTGAGATCTGAGGTGAT ACGATCGAGGAAGTC <del>A</del> CGAAGAGGTAAACGCCATGGAAGGATTGA AGGCCGTGTGGTGAAGCTTCAACGCCATTGCT	6738
		CCTCTCGT <del>G</del> ACTTCCT AGGAAGTC <del>A</del> CGAAGAGGTAA	6739 6740
20	Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Gly20Term GGA-TGA	TGGCTCTGAATCTCAACCCGTTCCACACCATTCACTGTCGTCG ATTGCCGTCTTCTGACCTCGTCAAACGCCCTCTCGCAGATCTCCC AAATTCTCATGGCTCCACTCTCAGCAG	6741
		CTGCTGAGAGTGGAGGCCATGAAGAATTGGGAGATCTGCGAGAA GGCGTTTGACGAGGT <del>C</del> AGAAAGACGGCAATCGACGACACTGAAAT	6742
		GGTGTGAAACGGGTTGAGATTCAAGAGCCA	
25	Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Ser21Term TCA-TGA		
30			

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Gln24Term CAA-TAA	GTCTTTCT <u>GACCTCGTC</u>	6743
		GACGAGGT <u>CAGAAAGAC</u>	6744
		AATCTCAACCCGTTCCACACCATT <u>CAGTGTGTCGATTGCCGT</u> CTTTCTCACCTCG <u>TAAACGCCTCTCGCAGATCTCCAAATTCTT</u> CATGGCTTCACTCT <u>CAGCAGCTTCTC</u>	6745
		GAGAAGAGCTGCTGAGAGTGGAA <u>GCCATGAAGAATTGGGAGATC</u> TGCGAGAAGGC <u>GTTAACGAGGTGAGAAAGACGGCAATCGACGA</u> CACTGAA <u>ATGGTGTGGAAACGGGTTGAGATT</u>	6746
		CACCTCG <u>TAAACGCCT</u>	6747
10	Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Arg29Term AGA-TGA	AGGC <u>GTTAACGAGGTG</u>	6748
		TCCACACCATT <u>CAGTGTGTCGATTGCCGT</u> AAACGCCTTCTCG <u>GATCTCCAAATTCTT</u> CATGGCTTCACTCT <u>CAGCAGCTTCTCCTAAGGAAGCGGAA</u>	6749
		TTTCCGCTCCT <u>TTAGGAGAAGAGCTGCTGAGAGTGGAAAGCCATGA</u> AGAATT <u>TTGGAGATCAGCGAGAAGCGTTGACGAGGTGAGAAAG</u> ACGGCAATCGACGACACT <u>GAAATGGTGTGGA</u>	6750
		CTTCTCG <u>GCTGATCTCC</u>	6751
		GGGAGAT <u>CAGCGAGAAG</u>	6752
15	Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Lys32Term AAA-TAA	TTTCAGTGTGTCGATTGCCGT <u>CTTCTCACCTCGTCAAACGCC</u> CTCGCAGAT <u>CTCCCTAAATTCTT</u> CATGGCTTCACTCT <u>CAGCAGCT</u> TTCTCCTAAGGAAGCGGAAAGCCTGAAGA	6753
		TCTTCAGGCTTCCGCT <u>CCCTT</u> TAGGAGAAGAGCTGCTGAGAGTGG AAGCCAT <u>GAAGAATTAGGGAGATCTGCAGAAGCGTTGACGAG</u> GTGAGAAAGACGGCAATCGACGACACTGAAA	6754
		GAT <u>CTCCCTAAATTCTT</u> C	6755
		GAAGAATT <u>AGGGAGATC</u>	6756
		AAATAGTC <u>GAGGTGAAAAACAGAGC</u> ATCAACAAT <u>GGCACTGAATAT</u> CAATGGGGTGT <u>CGTAAAATCTCACAAATGTTACCA</u> TTCC <u>TTCTCAGCCAGATCTGAGCGAGTTT</u> CAT	6757
20	Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu10Term TTA-TGA	ATGAAA <u>ACTCGCTCAGATCTGGCTGAAGAACACAAGGAAATGGTAACA</u> TTTG <u>TGAGATTTCACGACACCCATTGATATT</u> CAGTGCCATTGTT GATGCT <u>CTGTTTCACTCGACTATTT</u>	6758
		GGTGT <u>CGTGAAATCTC</u>	6759
		GAGATT <u>TCACGACACC</u>	6760

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys11Term AAA-TAA	ATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCA ATGGGGTGTGTTATAATCTCACAAATGTTACCATTCCTTGTCT TCAGCCAGATCTGAGCGAGTTTCATGG	6761
		CCATGAAAACTCGCTCAGATCTGGCTGAAGAACAGGAAATGGTA ACATTTGTGAGATTATAACGACACCCCATTGATATTCACTGCCATT GTTGATGCTCTGTTTACCTCGACTAT	6762
		TGTCGTTATAATCTCAC	6763
		GTGAGATTATAACGACA	6764
10	Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys14Term AAA-TAA	GTGAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGTGT CGTTAAAATCTCACTAAATGTTACCATTCCTTGTCTTCAGCCAGA TCTGAGCCAGTTTCATGGCTTCAACCA	6765
		TGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAAGAACAG GAAATGGTAACATTAGTGAGATTAAACGACACCCCATTGATATT AGTGCCATTGTTGATGCTCTGTTTAC	6766
		AATCTCACTAAATGTTA	6767
		TAACATTAGTGAGATT	6768
15	Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu16Term TTA-TGA	ACAGAGCATCAACAATGGCACTGAATATCAATGGGTGTGTTAAA ATCTCACAAATGTGACCATTCTTGTCTTCAGCCAGATCTGAG CGAGTTTCATGGCTTCAACCATTCTCG	6769
		CGATGAATGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAA GAACAAGGAAATGGT <del>CAC</del> ATTTGTGAGATTAAACGACACCCCATT TGATATTCACTGCCATTGTTGATGCTCTGT	6770
		CAAAATGT <del>G</del> ACCATTTC	6771
		GAAATGGT <del>C</del> ACATTTC	6772
20	Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser21Term TCA-TGA	TGGCTCTGAGGCTGAACCCCTAACCCCTCACAGAAGCTTTCTCTC TCCCTCTTCATCATGATCTCTCTTCATCGTTCTCGCTTC AAATGGCTAGCCTCAGATCTCCAAGGTT	6773
		AACCTTGGAGATCTGAGGCTAGCCATTGAGGAAGCGAGAACGAT GAAGAAGAAGAAGAT <del>C</del> ATGATGAAGAAGGAGAGAGAAAGAGCTTC TGTGAAGGGTTAGGGTTAGCCTCAGCCTCAGAGCCA	6774
		TTCATCATGATCTCTT	6775
		AAGAAGAT <del>C</del> ATGATGAA	6776
25	Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser26Term TCA-TGA	ACCCTAACCTTCACAGAAGCTTTCTCTCCTTCTCATCATCA TCTTCTTCTTCTTGTATCGTTCTCGCTTCAAATGGCTAGCCTCA GATCTCCAAGGTTCCGATGGCCTCCAC	6777
		GTGGAGGCCATGCGAACCTTGGAGATCTGAGGCTAGCCATTGA GGAAGCGAGAACGAT <del>C</del> AGAAGAAGAAGATGATGATGAAGAAGGA	6778
30		GAGAGAAAGAGCTCTGTGAAGGGTTAGGGT	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser27Term TCG-TAG	TTCTTCTT <u>GATCGTTCT</u>	6779
		AGAACGAT <u>CAAGAAGAA</u>	6780
		CTAACCCCTCACAGAACGCTTTCTCTCCTCTCATCATCATCT TCTTCTTCTTCAT <u>AGTTCTCGCTCCTCAAATGGCTAGCCTCAGAT</u> CTCCAAGGGTCCGCATGGCCTCCACCCT	6781
		AGGGTGGAGGCCATCGGAACCTGGAGATCTGAGGCTAGCCAT TTGAGGAAGCGAGAAC <u>ATATGAAGAAGAAGATGATGATGAAGA</u> AGGAGAGAGAAAGAGCTCTGTGAAGGGTAG	6782
		TTCTTCAT <u>AGTTCTCGC</u>	6783
		GCGAGAAC <u>ATATGAAGAA</u>	6784
	Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser29Term TCG-TAG	CTTCACAGAACGCTTTCTCTCCTCTCATCATCATCATCTTCT TCTTCATCGTT <u>CTAGCTCCTCAAATGGCTAGCCTCAGATCTCAA</u> GGTCCGCATGGCCTCCACCCTCCGCAC	6785
		GTGCGGAGGGTGGAGGCCATCGGAACCTGGAGATCTGAGGCT AGCCATTGAGGAAG <u>CTAGAACGATGAAGAAGAAGATGATGA</u> TGAAGAAGGAGAGAGAAAGAGCTCTGTGAAG	6786
		ATCGTT <u>CTAGCTCCTC</u>	6787
		GAGGAAG <u>CTAGAACGAT</u>	6788
		AAAGTTAAAGCCGTC AAGAAAAAATGGCT <u>TAAGAATT</u> TAATGCCATGCCCTCGAAATCTCA GAAGCTCCCTGCTTGCTCTCCACCAA	6789
15	Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Leu3Term TTG-TAG	TTGGTGGAAAGAGCAAAGCAAGGGAGCTCTGAGATTGAGGCG ATGGCATTAAATT <u>CTAAGCCATT</u> TTTCTTCTGGCTTGCCTTCC GGTTGGGTTTGGACGGCTTTAAC	6790
		AATGGCT <u>TAAGAATT</u> TA	6791
		TAAAATT <u>CTAAGCCATT</u>	6792
		CCCAAACCAGGAAAGGCAAACGAAAAGAAAAATGGCTTGAA TAATGCCATGCC <u>CTAGAAAT</u> CTCAGAACGCTCCCTGCTTGCTCTT CCACCAAAGGCCACCCCTAGATCTCCCAA	6793
		TTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAAAGCAAGG GAGCTTCTGAGATT <u>CTAGGCATGGCATT</u> AAAATTCAAAGCCATT TTTCTTCTGCTTGCCCTTCCCTGGTTGG	6794
20	Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Ser1-Term TCG-TAG	CATGCC <u>CTAGAAAT</u> CTC	6795
		GAGATT <u>CTAGGCATG</u>	6796

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Lys11Term AAA-TAA	CAAACCAGGAAAGGCAAACGAAAAGAAAAAATGGCTTGAATTTA ATGCCATCGCCTCGTAATCTCAGAAGCTCCCTGCTTGTCTTCC ACCAAAGGCCACCCCTAGATCTCCAAGT	6797
		ACTTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAAAGCAAG GGAGCTCTGAGATTACGAGGCCATGGCATTAAAATTCAAAGCCA TTTTTCTTTCGTTGCCTTCTGGTTTG	6798
		TCGCCTCGTAATCTCAG	6799
		CTGAGATTACGAGGCCA	6800
10	Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Gln13Term CAG-TAG	AGGAAAGGCCAACGAAAAGAAAAAATGGCTTGAATTTAATGCCA TCGCCTCGAAATCTTAGAAGCTCCCTGCTTGTCTTCCACCAA GGCCACCCCTAGATCTCCAAGTTTCCA	6801
		TGGAAAACCTGGGAGATCTAAGGGTGGCCTTGGTGGAAAGAGCAA AGCAAGGGAGCTCTAAGATTTCGAGGCCATGGCATTAAAATTCAA AGCCATTTTCTTTCGTTGCCTTCT	6802
		CGAAATCTAGAAGCTC	6803
		GAGCTTCTAAGATTCG	6804

**Table 24**  
**Oligonucleotides to produce plants with reduced linolenic acid**

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser4Term TCG-TAG	AATAGAACGACAGAGACTTTCTCTTCTTGGGAAGAGGC TCCAATGGCGAGCTAGGTTTATCAGAATGTGGTTAGACCTCTC CCCAGATTCTACCCCTAACACACACAAACCTC	6805
10		GAGGGTTGTGTAGGGTAGAATCTGGGGAGAGGTCTAAACCA CATTCTGATAAAACCTAGCTCGCCATTGGAGCCTCTCCCAAGAAG AAAAGAGGAAAAAGTCTCTGTCGTTCTATT	6806
		GGCGAGCTGGTTTAT	6807
		ATAAAACCAAGCTCGCC	6808
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Leu6Term TTA-TGA	ACGACAGAGACTTTCTCTTCTTGGGAAGAGGTCCAAT GGCGAGCTCGGTTTATCAGAATGTGGTTAGACCTCTCCCCAG ATTCTACCCCTAACACACACAAACCTCTTTGC	6809
		GCAAAAGAGGTTGTGTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGATCAAACCGAGCTCGCCATTGGAGCCTTCC CAAGAAGAAAAAGAGGAAAAAGTCTCTGTCGT	6810
		CTCGGTTTATGATCAGAAT	6811
		ATTCTGATCAAACCGAG	6812
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser7Term TCA-TGA	ACAGAGACTTTCTCTTCTTGGGAAGAGGTCCAATGGC GAGCTCGGTTTATGAGAATGTGGTTAGACCTCTCCCCAGATT TACCCCTAACACACACAAACCTCTTTGCCTC	6813
		GAGGCAAAAGAGGTTGTGTAGGGTAGAATCTGGGGAGAGG CTAAAACACATTCTATAAAACCGAGCTCGCCATTGGAGCCTT CCCAAGAAGAAAAAGAGGAAAAAGTCTCTGT	6814
		GGTTTATGAGAATGTG	6815
		CACATTCTATAAAACC	6816
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Glu8Term GAA-TAA	AGAGACTTTCTCTTCTTGGGAAGAGGTCCAATGGCGA GCTCGGTTTATCATAATGTGGTTAGACCTCTCCCCAGATTCTA CCCTAACACACACAAACCTCTTTGCCTCTA	6817
		TAGAGGCAAAAGAGGTTGTGTAGGGTAGAATCTGGGGAGAG GTCTAAAACACATTATGATAAAACCGAGCTCGCCATTGGAGCCTC TTCCCAAGAAGAAAAAGAGGAAAAAGTCTCT	6818
		TTTTATCATAATGTGGT	6819
		ACCACATTATGATAAAA	6820

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu4Term TTG-TAG	TCATCATCTCTCTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAAGCTTATCCGAATGTGGCATAAGACCTCTCCCCAGAACCCAGATCCAC	6821
		GTGGATCTGGGTGTGGTAGATTCTGGGGAGAGAGGTCTTATGCCACATTGGATAAGACCTAGTCGCCATTGCTAGAGCTCTTGTCTCTCTCCCCAGAACCCAGATCCAC	6822
		GGCGAACT <u>AGGTCTTAT</u>	6823
		ATAAGACCT <u>AGTTGCC</u>	6824
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu6Term TTA-TGA	TCTCTTCTCTGGGGAGAGAGAGAGAGCAAAAGAGCTTAGCAAAGATCCGAATGTGGCATAAGACCTCTCCCCGAATCTACACCACACCCAGATCCACTTTCTCCCC	6825
		AGGAAAGTGGATCTGGGTGTGGTAGATTCTGGGGAGAGGTCTTATGCCACATTGGAT <u>CAGACCAAGTTGCCATTGCTAGAGCTCTT</u> TGCTCTCTCTCTCCCCAGAACAGAAGAAGA	6826
		CTTGGTCT <u>GATCCGAAT</u>	6827
		ATTCGGAT <u>CAGACCAAG</u>	6828
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Glu8Term GAA-TAA	TTCTCTGGGGAGAGAGAGAGAGCAAAAGAGCTTAGCAATGGCGAACTGGTCTTATCCTAATGTGGCATAAGACCTCTCCCCAGAACATCTACACCACACCCAGATCCACTTTCTCTCCA	6829
		TGGAGAGGAAAGTGGATCTGGGTGTGGTAGATTCTGGGGAGAGGTCTTATGCCACATT <u>AGGATAAGACCAAGTTGCCATTGCTAGAG</u> CTCTTGTCTCTCTCCCCAGAACAGA	6830
		TCTTATCCTAATGTGGC	6831
		GCCACATT <u>AGGATAAGA</u>	6832
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Cys9Term TGT-TGA	CTGGGGAGAGAGAGAGAGCAAAAGAGCTTAGCAATGGCGAACTTGGTCTATCCGAATGAGGCATAAGACCTCTCCCCAGAACATCTACACACACCCAGATCCACTTTCTCTCCAACACCC	6833
		GGTGTGGAGAGGAAAGTGGATCTGGGTGTGGTAGATTCTGGGAGAGGTCTTATGCC <u>CATTGGATAAGACCAAGTTGCCATTGCTAGAGCTCTTGTCTCTCTCCCCAG</u>	6834
		TCCGAATG <u>AGGCATAAG</u>	6835
		CTTATGCC <u>CATTGGAA</u>	6836
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Trp5Term TGG-TGA	ATAACAGAATTGCTGAATTCTTGCATTTAGCTCTGGGTTTCAAAGAATCTACTCACGACCCAGAACATTGGT	6837
		ACCAATTCTGGGTGCGTAGAGTAGATTCTGGGAGAGGCCTTAAACCACATTCTGATAATACT <u>CAACCAAGCAGCCATTGAAACCCAGAACGCT</u> AAAAATGCAAGAATTAGCAATTCTGTTAT	6838

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Leu7Term TTA-TGA	GCTGGTTG <u>A</u> GTATTATC	6839
		GATAATA <u>C</u> CAACCAGC	6840
		AGAATTGCTGAATTCTGCATTTAGCTTCTGGGTTTCAATGGCT GCTGGTTGGGTATT <u>G</u> ATCAGAA <u>T</u> GTGGTTAAGGCCTCTCCCAAGA ATCTACTCAGCACCCAGAATTGGTTTAC	6841
		GTAAAACCAATTCTGGGT <u>C</u> GTGAGTAGATTCTGGGAGAGGCCTT AAACCACATTCTGAT <u>C</u> ATACCCAA <u>C</u> CCAGCAGCCATTGAAAACCAG AAGCTAAAATGCAAGAATT <u>C</u> AGCAATTCT	6842
		TTGGGTATT <u>G</u> ATCAGAAT	6843
		ATTCTGAT <u>C</u> ATACCCAA	6844
	Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Ser8Term TCA-TGA	ATTGCTGAATTCTGCATTTAGCTTCTGGGTTTCAATGGCTGCT GGTTGGGTATTAT <u>G</u> AGAA <u>T</u> GTGGTTAAGGCCTCTCCCAAGAATCT ACTCACGACCCAGAATTGGTTTACATC	6845
		GATGTAAAACCAATTCTGGGT <u>C</u> GTGAGTAGATTCTGGGAGAGGC CTTAAACCACATT <u>C</u> TAATACCCAA <u>C</u> CCAGCAGCCATTGAAAACC CAGAAGCTAAAATGCAAGAATT <u>C</u> AGCAAT	6846
		GGTATTAT <u>G</u> AGAA <u>T</u> GTG	6847
		CACATT <u>C</u> TAATACC	6848
		TGCTGAATTCTGCATTTAGCTTCTGGGTTTCAATGGCTGCTG GTTGGGTATTAT <u>C</u> ATA <u>T</u> GTGGTTAAGGCCTCTCCCAAGAATCTA CTCACGACCCAGAATTGGTTTACATCGA	6849
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Glu9Term GAA-TAA	TCGATGTAAAACCAATTCTGGGT <u>C</u> GTGAGTAGATTCTGGGAGAG GCCTTAAACCACATT <u>A</u> TGATAATACCCAA <u>C</u> CCAGCAGCCATTGAAA CCCAGAAGCTAAAATGCAAGAATT <u>C</u> AGCA	6850
		TATTAT <u>C</u> ATA <u>T</u> GTGGT	6851
		ACCACATT <u>A</u> TGATAATA	6852
		GCAAGTTGGGTTTATCAGAA <u>T</u> GTGGCTT <u>A</u> GACCA <u>C</u> CTCCAA <u>G</u> AA TCTACCC <u>C</u> TA <u>G</u> CC <u>C</u> T <u>G</u> AA <u>T</u> GTGGG <u>C</u> AG <u>C</u> CA <u>T</u> TC <u>G</u> C <u>C</u> T <u>C</u> TC ACATTA <u>A</u> GG <u>T</u> G <u>A</u> GA <u>A</u> TT <u>T</u> CA <u>C</u> GTACAG <u>A</u> TC	6853
		GATCTGTACGT <u>G</u> AA <u>A</u> TT <u>T</u> CA <u>A</u> CT <u>T</u> TA <u>A</u> GT <u>G</u> GAG <u>A</u> GG <u>A</u> GG <u>C</u> AG <u>A</u> GT GG <u>C</u> GT <u>G</u> CC <u>C</u> AG <u>T</u> TC <u>A</u> GG <u>G</u> CT <u>T</u> AG <u>GG</u> GT <u>A</u> TT <u>T</u> CT <u>GG</u> G <u>A</u> GT <u>GG</u> T <u>C</u> AAG <u>A</u> CC <u>A</u> CA <u>T</u> CT <u>G</u> ATA <u>AA</u> CC <u>C</u> AA <u>T</u> T <u>G</u> C	6854
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg22Term AGA-TGA	CTAAG <u>C</u> CC <u>T</u> GA <u>A</u> CT <u>GG</u> G	6855
		CCCAG <u>T</u> TC <u>AG</u> GG <u>G</u> CT <u>T</u> AG	6856

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Lys34Term AAG-TAG	CTCCAAGAACCTACCCCTAACGCCAGAACCTGGGGCAGCCACTTCTGCCT GCCTCCTCTCACATTAGTTGAGAACATTACGTACAGATCTGAGTG GTTCTGCAATTCTTGTCTAATACTAATA	6857
		TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACG TGAAATTCTCAACTAAATGTGAGAGGAGGCAGAAGTGGCTGCC AGTTCTGGCTTAGGGTAGATTCTGGGAG	6858
		CTCACATTAGTTGAGA	6859
		TCTCAACTAAATGTGAG	6860
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Leu35Term TTG-TAG	CAAGAACCTACCCCTAACGCCAGAACCTGGGGCAGCCACTTCTGCCT CCTCTCACATTAAAGTAGAGAACATTACGTACAGATCTGAGTG TGCAATTCTTGTCTAATACTAATAAAGA	6861
		TCTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGT ACGTGAAATTCTCTACTTAATGTGAGAGGAGGCAGAAGTGGCTGC CCCAGTTCTGGCTTAGGGTAGATTCTG	6862
		CATTAAGTAGAGAACATT	6863
		AAATTCTCTACTTAATG	6864
		AGAACCTACCCCTAACGCCAGAACCTGGGGCAGCCACTTCTGCCTCC TCTCACATTAAAGTAGTTGAAATTACGTACAGATCTGAGTG CAATTCTTGTCTAATACTAATAAAGAGA	6865
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg36Term AGA-TGA	TCTCTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCT GTACGTGAAATTCAACAATTAAATGTGAGAGGAGGCAGAAGTGGCT GCCCGAGTTCTGGCTTAGGGTAGATTCT	6866
		TTAAGTTGTGAATTCA	6867
		TGAAATTCAACAATTAA	6868
		GCGAGTTGGGTTTATCAGAACCTGGTCTGAGGCCACTCCGAGG GTCTATCCTAACGCCATGAACCTGGCCACCCCTTGTGAATTCCAATC CCACAAAGCTGAGATTTCAGAACAGATC	6869
		GATCTGTTCTGAAAATCTCAGCTTGTGGATTGAAATTCAACAA AGGGTGGCCAGTTCACTGGCTAGGATAGACCCCTGGGAGTGGCC TCAGACCACATTCTGATAAAACCAACTCGC	6870
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Arg22Term AGA-TGA	CTAACGCCATGAACCTGGC GCCAGTTCATGGCTTAG	6871 6872
		GCGAGTTGGGTTTATCAGAACCTGGTCTGAGGCCACTCCGAGG GTCTATCCTAACGCCATGAACCTGGCCACCCCTTGTGAATTCCAATC CCACAAAGCTGAGATTTCAGAACAGATC	6873
		GATCTGTTCTGAAAATCTCAGCTTGTGGATTGAAATTCAACAA AGGGTGGCCAGTTCACTGGCTAGGATAGACCCCTGGGAGTGGCC TCAGACCACATTCTGATAAAACCAACTCGC	6874
		CTAACGCCATGAACCTGGC GCCAGTTCATGGCTTAG	6875 6876
		GCGAGTTGGGTTTATCAGAACCTGGTCTGAGGCCACTCCGAGG GTCTATCCTAACGCCATGAACCTGGCCACCCCTTGTGAATTCCAATC CCACAAAGCTGAGATTTCAGAACAGATC	6877
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu27Term TTG-TAG	GATCTGTTCTGAAAATCTCAGCTTGTGGATTGAAATTCAACAA AGGGTGGCCAGTTCACTGGCTAGGATAGACCCCTGGGAGTGGCC TCAGACCACATTCTGATAAAACCAACTCGC	6878
		CTAACGCCATGAACCTGGC GCCAGTTCATGGCTTAG	6879 6880
30	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu27Term TTG-TAG	GATCTGTTCTGAAAATCTCAGCTTGTGGATTGAAATTCAACAA AGGGTGGCCAGTTCACTGGCTAGGATAGACCCCTGGGAGTGGCC TCAGACCACATTCTGATAAAACCAACTCGC	6881
		CTAACGCCATGAACCTGGC GCCAGTTCATGGCTTAG	6882 6883

	Phenotype Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
		CCACCCTT <u>A</u> GTTGAATT	6875
		AATTCAACT <u>A</u> AGGGTGG	6876
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu28Term TTG-TAG	AATGTGGCTTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAA CTGGCCACCCCTTGT <u>A</u> GAATTCCAATCCCACAAAGCTGAGATTTC AAGAACAGATCTTGGAAATGGTTCTTCATT	6877
		AATGAAGAACCATTTCAAGATCTGTTCTGAAAATCTCAGCTTGT GGGATTGGAATTCT <u>A</u> CAAAGGGTGGCCAGTTCTGGCTTAGGATA GACCCTCGGGAGTGGCCTCAGACCACATT	6878
		CCCTTTGT <u>A</u> GAATTCCA	6879
		TGGAATTCT <u>A</u> CAAAGGG	6880
		CTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCCTTGTG AATTCCAATCCCACAT <u>A</u> GCTGAGATTTCAAGAACAGATCTGGAA ATGGTTCTTCATTCTGTTGTGAGTGGGA	6881
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Lys34Term AAG-TAG	TCCCACACTGACAAACAGAACATGAAGAACCATTTCAAGATCTGTTCT TGAAAATCTCAGCT <u>A</u> TGTGGATTGGAATTCAACAAAGGGTGGCC AGTTCTGGCTTAGGATAGACCCCTGGGAG	6882
		ATCCCACAT <u>A</u> GCTGAGA	6883
		TCTCAGCT <u>A</u> TGTGGGAT	6884
		CATCAGAGCGCGATACCTAACGCATTGCTGGGTTAAGAACATCCATG GAAGTCTATGAGTTAGGTCGTCAAGAGAGCTAGCCATCGTGTTCGC ACTAGCTGCTGGAGCTGCTTACCTAACAAAT	6885
		ATTGTTGAGGTAAAGCAGCTCCACGAGCTAGTGCAGAACACGATGGC TAGCTCTCTGACGAC <u>C</u> TAACTCATAGACTCCATGGATTCTAACCC CAGCAATGCTTAGGTATGCCGCTCTGATG	6886
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Tyr3Term TAC-TAG	ATGAGTT <u>A</u> GGTCGTAG	6887
		CTGACGAC <u>C</u> TAACTCAT	6888
		GCAGCGATACCTAACGCATTGCTGGGTTAAGAACATCCATGGAAAGTCT ATGAGTTACGTCGT <u>C</u> TGAGAGCTAGCCATCGTGTTCGCACTAGCT GCTGGAGCTGCTTACCTAACAAATTGGCTTG	6889
		CAAGCCAATTGTTGAGGTAAAGCAGCTCCACGAGCTAGTGCAGAAC CGATGGCTAGCTCT <u>C</u> AGACGACGTAACTCATAGACTCCATGGAT TCTTAACCCAGCAATGCTTAGGTATGCCGC	6890
		ACGTCGT <u>C</u> TGAGAGCTA	6891
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Arg6Term AGA-TGA	TAGCTCT <u>C</u> AGACGACGT	6892

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Glu7Term GAG-TAG	GCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCTATGA GTTACGTCGTAGATAGCTAGGCCATCGTGTGCACTAGCTGCTG GAGCTGCTTACCTAACAAATTGGCTTGT	6893
		AAACAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCAG ACACGATGGCTAGCTATCTGACGACGTAACCTCATAGACTTCCATG GATTCTAACCCAGCAATGCTTAGGTATCGC	6894
		TCGTCAGATAGCTAGCC	6895
		GGCTAGCTATCTGACGA	6896
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Gly17Term GGA-TGA	CCATGGAAGTCTATGAGTTACGTCGTAGAGAGCTAGCCATCGTG TTCGCACTAGCTGCTTGAGCTGCTTACCTAACAAATTGGCTTGT GGCCTCTCTATTGGATTGCTCAAGGAACCA	6897
		TGGTTCCCTTGAGCAATCCAATAGAGAGGCCAACAAAGCCAATTGTT GAGGTAAGCAGCTCAAGCAGCTAGTGCGAACACGATGGCTAGCT CTCTGACGACGTAACCTCATAGACTTCCATGG	6898
		TAGCTGCTTGAGCTGCT	6899
		AGCAGCTCAAGCAGCTA	6900
		GCAAGTTGGGTTCTATCAGAATGTGGCTTAGACCACTACCAAGAA TATACCCCAAGCCCTGAATAGGGTCTTCTCGTTGCGCCACCAA TTAAATCTGAGAAGAATTTCACCTTCAC	6901
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg22Term AGA-TGA	GTGAAGGTGAAATTCTCTCAGATTAAATTGGTGGCGAACCGGA AGAAGACCCCTATTCAAGGGCTTGGGTATATTCTGGTAGTGGCTA AGACCACATTCTGATAGAACCCAACTTGC	6902
		CAAAGCCCTGAATAGGG	6903
		CCCTATTCAAGGGCTTGT	6904
		TGGTCTTAGACCACTACCAAGAATATACCCAAAGCCCAGAATAGG GTCTTCTTCCGTTGAGCCACCAATTAAATCTGAGAAGAATTCA CCTTCACCTATACGAAACAGATCGGAATTGT	6905
		ACAATTCCGATCTGTTGTAGGTGAAGGTGAAATTCTCTCAGA TTAAATTGGTGGCTAAACGGAGAACCCCTATTCTGGCTTGG GGTATATTCTGGTAGTGGCTAAGACCA	6906
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Cys29Term TGC-TGA	TCCGTTGAGCCACCAA	6907
		TTGGTGGCTCAAACCGGA	6908
		CACTACCAAGAATATACCCAAAGCCCAGAATAGGGCTTCCGT	6909
		TTGCGCCACCAATTGAAATCTGAGAAGAATTACCTTCACCTATA CGAACAGATCGGAATTGTTGGGCATTGAG	
		CTCAATGCCAACAAATTCCGATCTGTTGTAGGTGAAGGTGAAA TTCTTCTCAGATTCAATTGGTGGCGAACCGGAAGAACCCCTAT TCTGGGCTTGGGTATATTCTGGTAGTG	6910
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Leu33Term TTA-TGA		
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligo	SEQ ID NO.
	CACCAATT <u>GAAAT</u> CTGA	6911
	TCAGATT <u>CAATT</u> GGTG	6912
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg36Term AGA-TGA	AGAATATA <u>CCCAAAGCCCAGAATAGGGTCTTC</u> CGTTGCCA CCAATTAA <u>ATCTG</u> TGAAGAATT <u>CACCTCACCTACG</u> AACAGAT CGGAATTGGTGGGCATTGAGGGTAAGTG	6913
	CACTTACCC <u>TCATGCCAACAATTCCGATCTG</u> TCGTATAGGTGA AGGTGAA <u>ATTCTTC</u> ACAGATTA <u>ATTGGTGGCGAAACGGAAGAA</u> GACCCTATT <u>CTGGGCTTGGGTATATTCT</u>	6914
	TAA <u>ATCTG</u> TGAAGAATT	6915
	A <u>ATTCTTC</u> ACAGATT	6916
	CTCTTTTAT <u>ATCCTCC</u> CTT <u>CTTG</u> TTTGAG <u>TTCTGAGTCACC</u> TATGGCAAG <u>TTGAGT</u> GATT <u>TCAGAATGTGGCTAAGGCCACTTCC</u> AAGAAT <u>CTATGCCAGGCCAGAAGTGG</u> A	6917
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Trp4Term TGG-TGA	TCCACTT <u>CTGGGC</u> CTGGC <u>ATAGATTCTGGAAGTGGCCTAGCCC</u> ACATT <u>CTGAAATCAC</u> <u>CACTGCCATAGGTGACTCAGAACTCAA</u> AAAA <u>ACAAAGAAGAGGAGGATAATAAAGAG</u>	6918
	GCAAG <u>TTGAGT</u> GATT <u>TC</u>	6919
	GAA <u>ATCAC</u> <u>CACTTG</u> C	6920
	TAT <u>CCTCC</u> CTT <u>CTTG</u> TTTGAG <u>TTCTGAGTCACCTATGGCA</u> AG <u>TTGGGTGATT</u> <u>TGAGAATGTGGCTAAGGCCACTCCAAGAAC</u> T TATGCC <u>AGGCC</u> CCAGAAG <u>GTGGAGCTTCATG</u>	6921
	CATGAAG <u>CTCC</u> ACTT <u>CTGGGC</u> CTGGC <u>ATAGATTCTGGAAGTGGC</u> CTTAG <u>CCCACATTCT</u> <u>CAATCACCCAACTGCCATAGGTGACTCAG</u> AACT <u>CAAAAAAAACAAAGAAGAGGAGGATA</u>	6922
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Ser7Term TCA-TGA	GGT <u>GATT</u> <u>TGAGAATGTG</u>	6923
	CAC <u>ATTCT</u> <u>CAATCAC</u> C	6924
	T <u>CCTC</u> CT <u>CTT</u> <u>CTTG</u> TTTGAG <u>TTCTGAGTCACCTATGGCAAG</u> TTGGGT <u>GATT</u> <u>TCAATGTGGCTAAGGCCACTCCAAGAAC</u> AT <u>CTAT</u> GCC <u>AGGCC</u> CCAGAAG <u>GTGGAGCTTCATG</u> TT	6925
	AACATGAAG <u>CTCC</u> ACTT <u>CTGGGC</u> CTGGC <u>ATAGATTCTGGAAGTG</u> GCCT <u>TAGCCCACATT</u> <u>TGAAATCACCCAACTGCCATAGGTGACTC</u> AGAA <u>CTCAAAAAAAACAAAGAAGAGGAGG</u> GA	6926
	T <u>GATT</u> <u>TCAATGTGGG</u>	6927
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Glu8Term GAA-TAA	CCCAC <u>ATT</u> <u>TGAAATCA</u>	6928

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Cys9Term TGT-TGA	CTCTTCTTGT <del>TTT</del> TGAGTTCTGAGTCACCTATGGCAAGTTGGG TGATTCAGAATG <del>A</del> GGGCTAAGGCCACTCCAAGAATCTATGCCA GGCCCAGAAGTGGAGCTTCATGTTCAAC	6929
		GTTGAAACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGG AGTGGCCTTAGCCC <del>T</del> CATTCTGAAATACCCAACTGCCATAGGTG ACTCAGAACTCAAAAAAAACAAAGAAGAG	6930
		TCAGAATG <del>A</del> GGGCTAAG	6931
		CTTAGCCCC <del>T</del> CATTCTGA	6932
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Lys21Term AAA-TAA	ATGAAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTA ATGG <del>TTT</del> CATGCT <del>T</del> AAGAAGAAGAAGAAGAGGATTTCGACTT AAGCAATCCTCCTCCATTCAATATTGGTC	6933
		GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTC TTCTTCTTCTTCTT <del>A</del> AGCATGAAAACCATTAAACGCCATTAGAATTG GGGTGTCTTGTACTGTTGCTGCTTCAT	6934
		TTCATGCT <del>T</del> AAGAAGAA	6935
		TTCTTCTT <del>A</del> AGCATGAA	6936
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu22Term GAA-TAA	AAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATG G <del>TTT</del> CATGCT <del>A</del> AA <del>T</del> AAGAAGAAGAAGAAGAGGATTTCGACTTAAG CAATCCTCCTCCATTCAATATTGGTCAGA	6937
		TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTC TTCTTCTTCTTCTT <del>A</del> TTAGCATGAAAACCATTAAACGCCATTAGAA TTGGGGTGTCTTGTACTGTTGCTGCTT	6938
		ATGCTAA <del>A</del> TAAGAAGAA	6939
		TTCTTCTT <del>A</del> TTAGCAT	6940
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu23Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCT <del>A</del> AGA <del>A</del> TAAGAAGAAGAAGAGGATTTCGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6941
		GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTT <del>A</del> TTCTTAGCATGAAAACCATTAAACGCCATTAA GAATTGGGGTGTCTTGTACTGTTGCTG	6942
		CTAAAGA <del>A</del> TAAGAAGAA	6943
		TTCTTCTT <del>A</del> TTCTTAG	6944
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu24Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCT <del>A</del> AGA <del>A</del> TAAGAAGAAGAAGAGGATTTCGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6945
		GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTT <del>A</del> TTCTTAGCATGAAAACCATTAAACGCCATTAA GAATTGGGGTGTCTTGTACTGTTGCTG	6946
30			

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CTAAAGAATAAGAAGAA	6947
	TTCTTCTT <u>ATT</u> CTT <del>TT</del> AG	6948
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Tyr21Term TAT-TAG	GGTCCAAGCACAGCCTCTACAACATGTTGGTAATGGTGCAGGGAA AGAAGATCAAGCTTAGTTGATCCAAGTGCTCCACCACCCCTCAAG ATTGCAAATATCAGAGCAGCAATTCCAAA TTTGGAAATTGCTGCTCTGATATTGCAATCTTGAAGGGTGGTGGAA GCACTTGGATCAA <u>ACT</u> AAAGCTTGAAGCTTGTCTCCCTGCACCATTAC CAACATGTTAGAGGGCTGTGCTTGGACC CAAGCTTAG <u>TTT</u> GATCC	6949 6950 6951 6952
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Lys31Term AAG-TAG	GGTAATGGTGCAGGGAAAGAAGATCAAGCTTATTGATCCAAGTG CTCCACCAACCCCTCTAGATTGCAAATATCAGAGCAGCAATTCCAAA ACATTGCTGGAGAAGAACACATTGAGAT ATCTCAATGTGTTCTCTCCAGCAATGTTGGAAATTGCTGCTCT GATATTGCAAT <u>CT</u> AGAAGGGTGGTGGAGCACTTGGATCAAATAA GCTTGATCTCTTCCCTGCACCATTACC CACCCCT <u>CT</u> AGATTGCA TGCAAT <u>CT</u> AGAAGGGTG	6953 6954 6955 6956
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Arg36Term AGA-TGA	AAAGAAGATCAAGCTTATTGATCCAAGTGCTCCACCACCCCTCA AGATTGCAAATAT <u>CT</u> GAGCAGCAATTCCAAAACATTGCTGGAGAA GAACACATTGAGATCTGAGTTATGTT GAACATAACTCAGAGATCTCAATGTGTTCTCCAGCAATGTTT GGAATTGCTGCT <u>CA</u> AGATATTGCAATCTTGAAGGGTGGTGGAGCA CTTGGATCAAATAAGCTTGTATCTTCTT CAAATAT <u>CT</u> GAGCAGCA TGCTGCT <u>CA</u> AGATATTG	6957 6958 6959 6960
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Leu41Term AAA-TAA	TATTTGATCCAAGTGCTCCACCACCCCTCAAGATTGCAAATATCA GAGCAGCAATT <u>CC</u> <u>CA</u> AAACATTGCTGGGAGAAGAACACATTGAGATC TCTGAGTTATGTTCTGAGGGATGTGTTGG CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTGTTCTT CTCCCAGCAATGTT <u>AT</u> GGAAATTGCTGCTGTATTTGCAATCTTGA AAGGGTGGTGGAGCACTTGGATCAAATA CAATT <u>CC</u> <u>CA</u> AAACATTGC GCAATGTT <u>AT</u> GGAAATTG	6961 6962 6963 6964

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Glu8Term GAG-TAG	CATCCACCCGCACCCGCACCCGCCCGCTGACGGCGGGCAATGGC CCGGCTCGTGTCTCC <del>T</del> AGTGTCTCGGGCCTCGCCGCCGTCCGCC GCCTGCGCGCCGGCCGGGCGCCATTGCGGC GCGCCGCAATGGCGCCCCGGCCGGCGCAGGCGGCGGACGG GCGCGAGGCCGAGCACT <del>A</del> GGAGAGCACGAGCCGGGCCATTGC CGCCGTAGCGGGCGGGTGCGGGTGCGGGTGGATG	6965
		TGCTCTCC <del>T</del> AGTGCTCG	6967
		CGAGCACT <del>A</del> GGAGAGCA	6968
		ACCCGCACCCGCACCCGCCCGCTGACGGCGGGCAATGGCCCG CTCGTGTCTCCGAGTG <del>A</del> TCGGGCCTCGCGCCCGTCCGCCGC GCGCGCCGGCCGGGCGCCATTGCGGCCGGTCA	6969
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Cys9Term TGC-TGA	TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCAGGCGGCG ACGGGCGCGAGGCCG <del>A</del> TCACTCGGAGAGCACGAGCCGGCCA TTGCCGCCGTAGCGGGCGGGTGCGGGTGCGGGTGCGGGT	6970
		TCCGAGTG <del>A</del> TCGGGCCT	6971
		AGGCCCG <del>A</del> TCACTCGGA	6972
		CCGCACCCGCACCCGCCCGCTGACGGCGGGCAATGGCCCG CGTGCTCTCCGAGTG <del>C</del> AGGGCCTCGCGCCCGTCCGCCGC GCGCGGGCCGGGCGCCATTGCGGCCGGTAC	6973
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser10Term TCG-TAG	GGTGACCCGCCGCAATGGCGCCCCGGCCGGCGCAGGGGGC GGACGGGCGCGAGGCC <del>T</del> AGCACTCGGAGAGCACGAGCCGGC CATTGCCGCCGTAGCGGGCGGGTGCGGGTGCGGG	6974
		CGAGTGCT <del>A</del> GGGCCTCG	6975
		CGAGGCC <del>C</del> TAGCACTCG	6976
		GCTCGGGCTCGCGCCCGTCCGCCGCTGCGGCCGGGGGG CGCCATTGCGCGCGGTGACCCCCCGCGCTCTCCGCC CGCGTGTCCCGCGTCCCG <del>T</del> CATCCACCGCGA	6977
20	Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser29Term TCA-TGA	TCGCGGTGGATGGACCGGGACCGGGACGGCGCGGGCC CGGAGAGCGCGGGGGGT <del>C</del> ACCGCGCCGCAATGGCGCCCCGGCC GGCGCGCAGGCGGGACGGCGCGAGGCCGAGC	6978
		GGCGCGGT <del>G</del> ACCCCCCG	6979
		CGGGGGGT <del>C</del> ACCGCGCC	6980
		CCCCCTCCCCCACGCACACGCACAGATCCATCCGCC CCCCGCAATGAGGCC <del>G</del> TAGCAGGAGGCCAGCTGCAAGGCCACC GAGGACCAACCGCTCGAGTTGACGCCCAAGC	6981
25	Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu8Term GAG-TAG	GCTTGGCGGCGTGA <del>A</del> CTGGAGCGGGTGGTCTCGGTGGCCTTG CAGCTGCCCTCTGCT <del>A</del> GGCCTCATTGCGGGGCCATGGCCGC	6982
		GGATGGATCTGTGCGTGTGCGTGGGGAGGGGG	

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligo	SEQ ID NO:
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Gln9Term CAG-TAG	TGAGGCCGTAGCAGGAG	6983
		CTCCTGCTACGGCCTCA	6984
		CCTCCCCACGCACACGCACAGATCCATCCGCCATGGCCCC CGCAATGAGGCCGGAGTAGGAGGCAGCTGCAAGGCCACCGAG GACCACCGCTCCGAGTCGACGCCCAAGCCGC	6985
		GCGGCTTGGCGGCGTCGAACACTGGAGCGGTGGTCTCGGTGGC CTTGCAGCTCGCCTCTACTCCGGCCTCATTGCGGGGGCCATGG CCGGGATGGATCTGCGTGTGCGTGGGGGAGG	6986
		GGCCGGAGTAGGAGGCG	6987
		CGCCTCCTACTCCGGCC	6988
	Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu10Term GAG-TAG	CCCCCACGCACACGCACAGATCCATCCGCCATGGCCCCCGC AATGAGGCCGGAGCAGTAGGCGAGCTGCAAGGCCACCGAGGACC ACCGCTCCGAGTCGACGCCCAAGCCGC	6989
		GCGGCGGCTTGGCGGCGTCGAACACTGGAGCGGTGGTCTCGGT GGCCTTGCAGCTCGCCTACTGCTCCGGCCTCATTGCGGGGGCCA TGGCCGGGATGGATCTGCGTGTGCGTGGGG	6990
		CGGAGCAGTAGGCGAGC	6991
		GCTCGCCTACTGCTCCG	6992
		ACGCACAGATCCATCCGCCATGGCCCCCGCAATGAGGCCGG AGCAGGAGGCCGGAGCTGAAGGCCACCGAGGACCACCGCTCCGA GTTGACGCCGCCAGCCGCCCTCCGCATC	6993
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Cys13Term TGC-TGA	GATGCGGAAGGGCGGCGGCTGGCGCGTCGAACACTGGAGCGG TGGTCCTCGGTGGCCTTCAAGCTCGCCTCTGCTCCGGCCTCATT GCGGGGGGCCATGGCCGGATGGATCTGCGT	6994
		GCGAGCTGAAGGCCAC	6995
		GTGGCCTTCAAGCTCGC	6996
		CTTCACAAATCACAAATCGGAATCAGATCCACCAAGACACCCGG CGGCAATGGCGGCGTAGGGCACCCAGGAGGCCACTGCAAGGC TTCCGAGGACGCCCTCTCTTCGACGCC	6997
		GCGGCGTCGAAGAAGAGACGGCGTCCTCGGAAGGCCCTGCAGTC GGCCTCCTGGGTGCCCTACGCCGCCATTGCCGCCGGGTGCGT GGTGGATCTGATTCCGATTGTGATTGTGAAG	6998
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Ser4Term TCG-TAG	GGCGGCGTAGGCCACCC	6999
		GGGTGCGCTACGCCGCC	7000

	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Gln7Term CAG-TAG	ATCACAAATCGGAATCAGATCCACCA CGACACCCCGGCGGCAATG GCGGCGTCGGCGACCTAGGAGGCCACTGCAAGGCTTCCGAGG ACGCCCGTCTCTTCGACGCCGCCAAGCCCC	7001
		GGGGCTTGGCGGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGC CTTGCAGTCGGCCTCCTAGGTGCCGACGCCGCCATTGCCGCCG	7002
		GGGTGTCTGGTGGATCTGATTCCGATTGTGAT	7003
		CGGCGACCTAGGAGGCC	7004
		GGCCTCCTAGGTGCCG	7004
10	Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Glu8Term GAG-TAG	ACAAATCGGAATCAGATCCACCA CGACACCCCGGCGGCAATGGC GGCGTCGGCGACCCAGTAGGCCGACTGCAAGGCTTCCGAGGACG CCCGTCTCTTCGACGCCGCCAAGCCCCGC	7005
		GCGGGGGCTTGGCGGCCTCGAAGAAGAGACGGGCGTCCTCGGA AGCCTTGAGTCGGCCTACTGGTCGCCGACGCCGCCATTGCCG	7006
		CCGGGGTGTCTGGATCTGATTCCGATTGT	7007
		CGACCCAGTAGGCCGAC	7008
		GTCGGCCTACTGGTCG	7008
15	Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Cys10Term TGC-TGA	TCAGATCCACCA CGACACCCCGGCGGCAATGGCGCGTCGGCGA CCCAAGGAGGCCGACTGAAAGGCTTCCGAGGACGCCGTCTCTC TTCGACGCCGCCAAGCCCCGCCCTCCGCATC	7009
		GATGCGGAAGGGGGGGCTTGGCGGCCGTCGAAGAAGAGACGG GCGTCCTCGGAAGCCTTICAGTCGGCCTCTGGTCGCCGACGC	7010
		CGCCATTGCCGCCGGGTGTCGTGGATCTGA	7011
		GCCGACTGAAAGGCTTC	7011
		GAAGCCTTICAGTCGGC	7012

## WHAT IS CLAIMED IS:

1. An oligonucleotide for targeted alteration of genetic sequence, comprising a single-stranded oligonucleotide having a DNA domain, said DNA domain having at least one mismatch with respect to the genetic sequence to be altered, and further comprising chemical modifications of the oligonucleotide, said chemical modifications selected from the group consisting of an o-methyl modification, an LNA modification including LNA derivatives and analogs, two or more phosphorothioate linkages on a terminus, and a combination of any two or more of these modifications.
2. The oligonucleotide according to claim one that comprises two or more phosphorothioate linkages on at least the 3' terminus.
3. The oligonucleotide according to claim one that comprises a 2'-O-methyl analog.
4. The oligonucleotide according to claim one that comprises an LNA nucleotide, including an LNA derivative or analog.
5. The oligonucleotide according to claim one that comprises a combination of at least two modifications selected from the group of a phosphorothioate linkage, a 2'-O-methyl analog, a locked nucleotide analog and a ribonucleotide.
6. The oligonucleotide according to any one of claims 1 to 5 that comprises at least one unmodified ribonucleotide.
7. The oligonucleotide according to any one of claims 1 to 6, wherein the sequence of said oligonucleotide is selected from the group consisting of SEQ ID NOS: 4341-7012 .
8. A method of targeted alteration of genetic material, comprising combining the target genetic material with an oligonucleotide according to any one of claims 1 to 7 in the presence of purified proteins.

9. A method of targeted alteration of genetic material, comprising administering to a cell extract an oligonucleotide of any one of claims 1 to 7.

10. A method of targeted alteration of genetic material, comprising administering to a cell an oligonucleotide of any one of claims 1 to 7.

11. A method of targeted alteration of genetic sequence in callus, comprising administering to the callus an oligonucleotide of any one of claims 1 to 7.

12. A method of targeted alteration of genetic sequence, comprising combining target genetic material with an oligonucleotide according to any one of claims 1 to 7, said target genetic material being a non-transcribed DNA strand of a duplex DNA.

13. The genetic material obtained by any one of the methods of claim 8, 9 or claim 10.

14. A cell comprising the genetic material of claim 13.

15. A plant organism comprising the cell according to claim 14.

16. A plant or plant part produced by the method of claim 11.

17. A method of determining whether an oligonucleotide is optimized for targeted alteration of a genetic sequence, which comprises:

(a) comparing the efficiency of alteration of a targeted genetic sequence by an oligonucleotide of any one of claims 1 to 7 with the efficiency of alteration of the same targeted genetic sequence by a second oligonucleotide, said second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2'-O-methylated oligonucleotide and a chimeric double-stranded double hairpin containing RNA and DNA nucleotides.

- 205 -

18. The method of claim 17 in which the alteration is produced in a plant cell extract
19. The method of claim 17 in which the alteration is produced in a cell.
20. A kit comprising the oligonucleotide according to any one of claims 1 to 7 and a second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2-O-methylated oligonucleotide and a chimeric double stranded double hairpin containing RNA and DNA nucleotides.

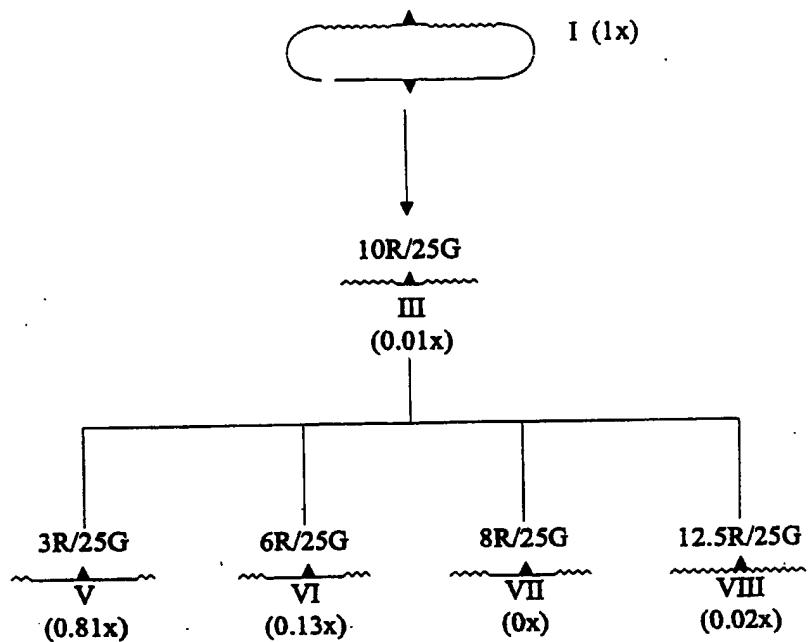


Figure 1A

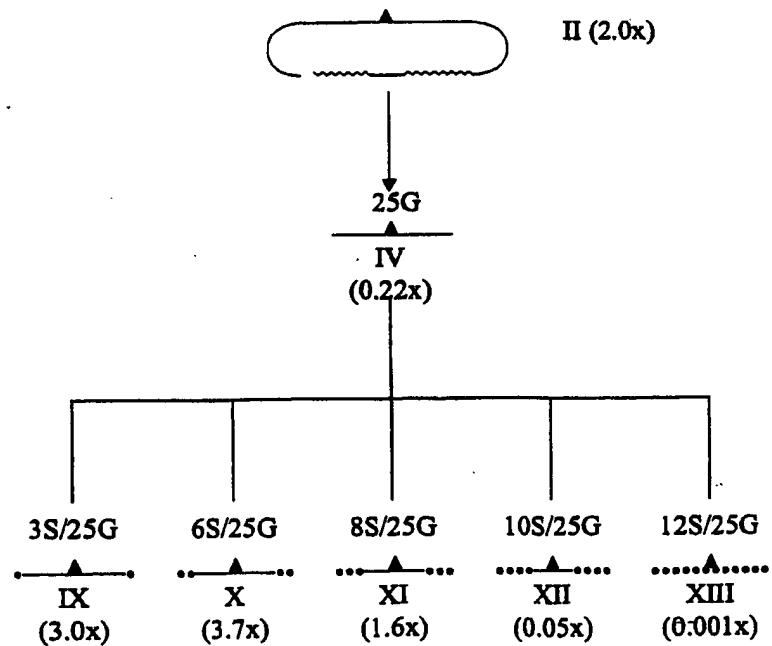


Figure 1B

## Plasmids, DNA targets and chimeric oligonucleotides

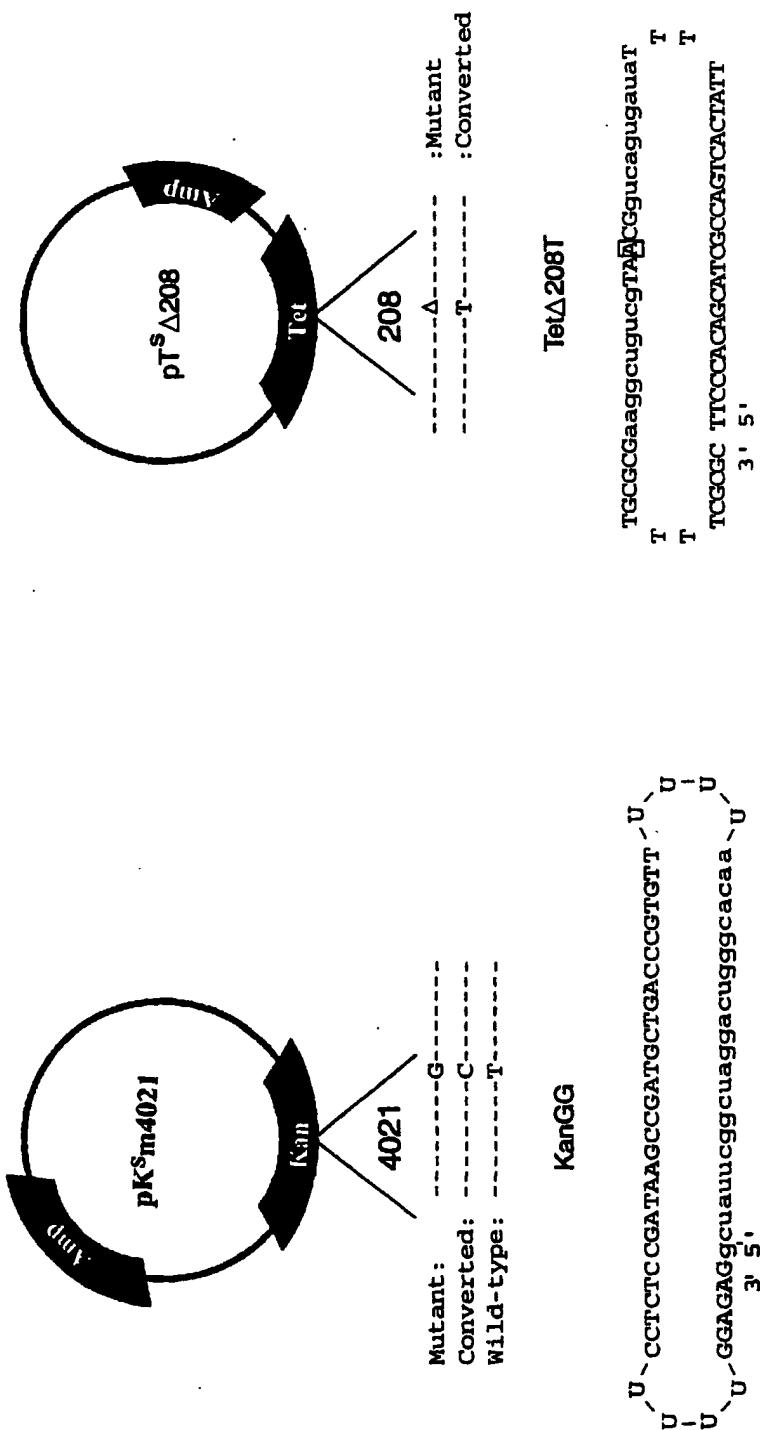


Figure 1C

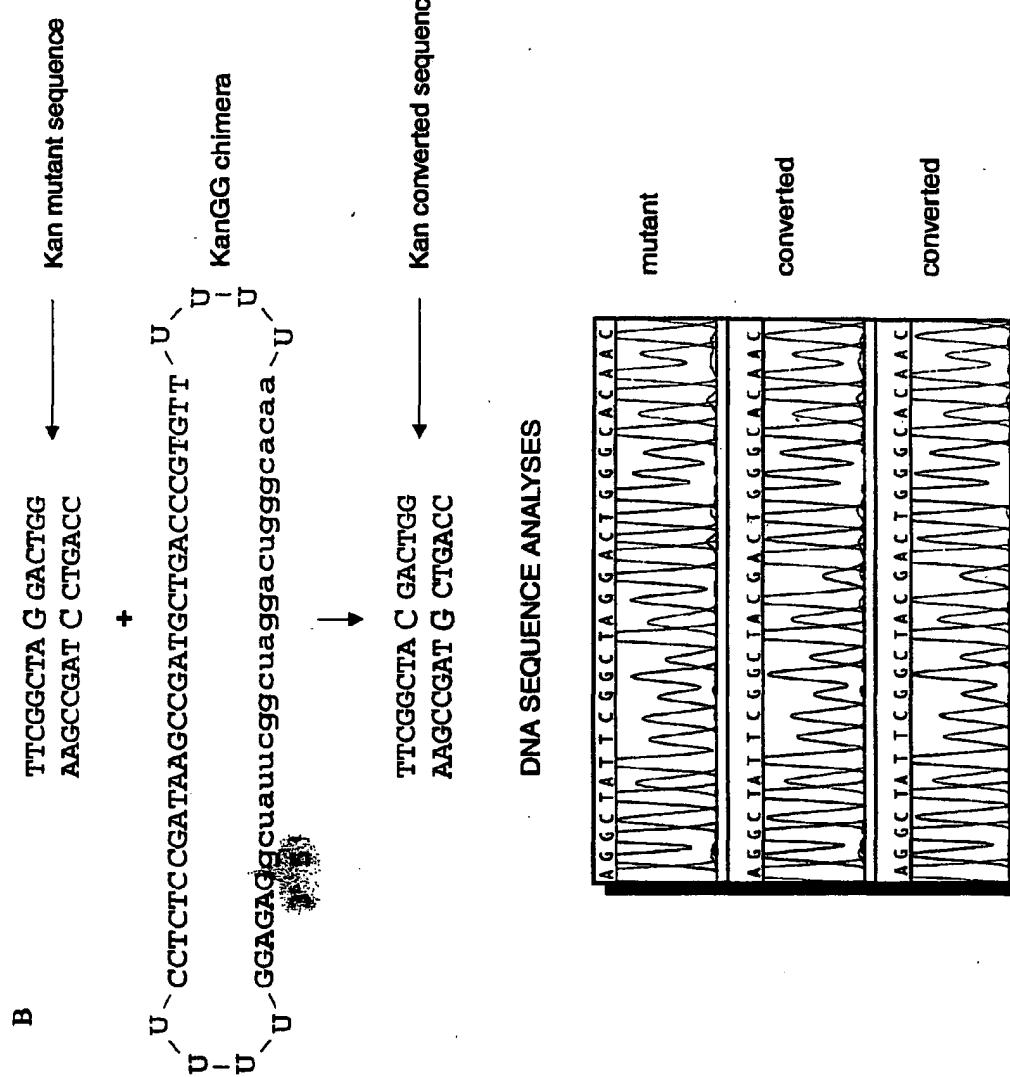


Figure 1D

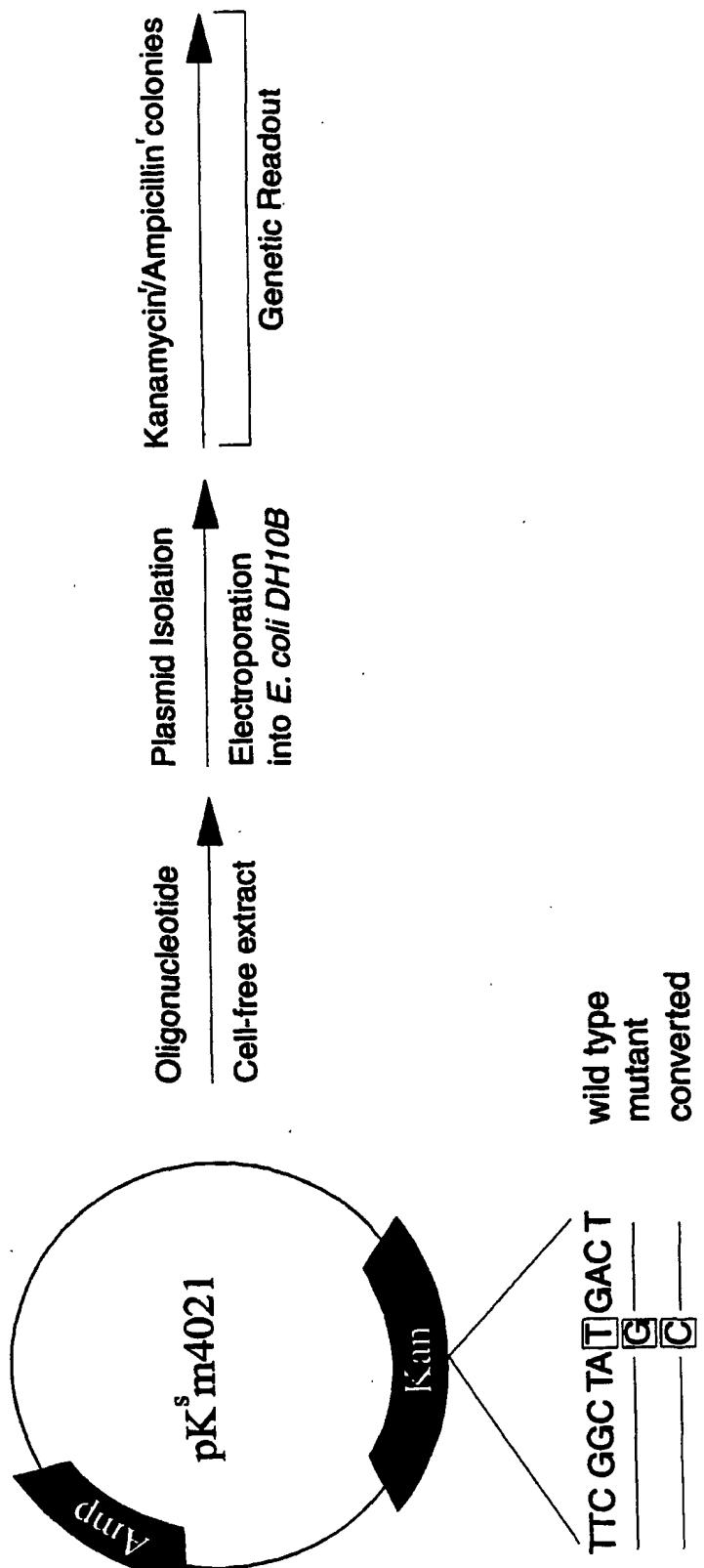
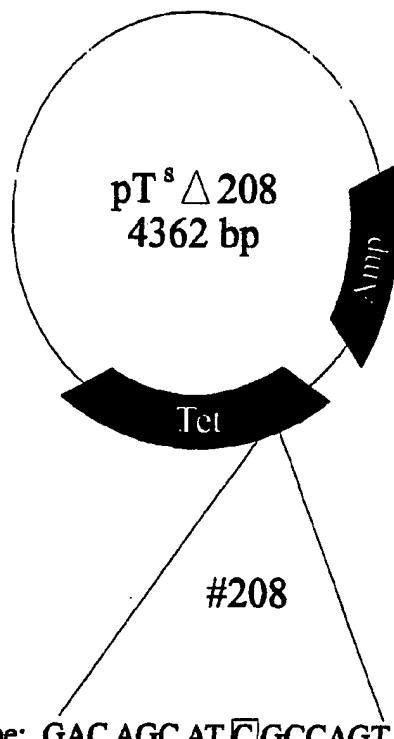


Figure 2



#208

Wild type: GAC AGC AT **C** GCCAGT  
 Mutant: GAC AGC AT - GCCAGT  
 Converted: GAC AGC AT **T** GCCAGT

### Sequence analysis of Tet<sup>r</sup> plasmid Δ208

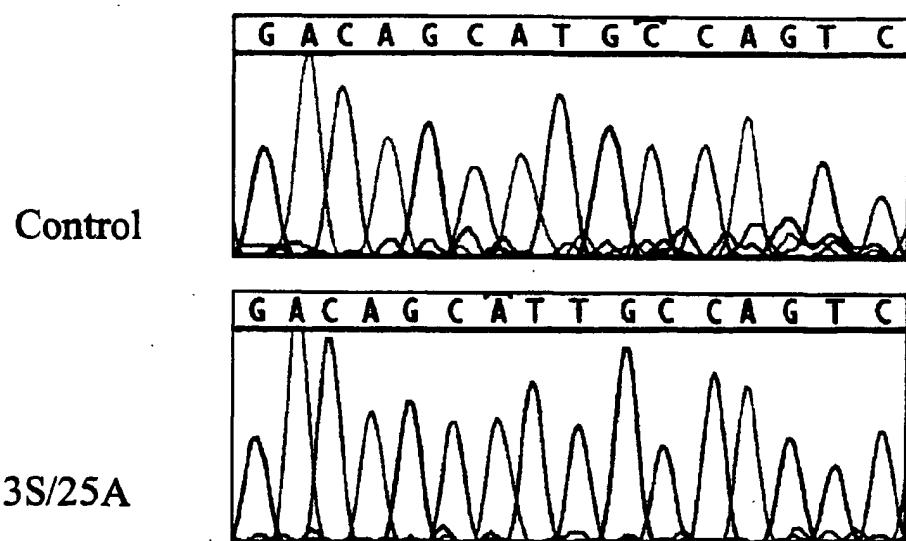


Figure 3

## DNA sequence analysis of Kan<sup>r</sup> plasmids

Target codon distribution					
oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)	---	+	---	---	---
2) 6S/25G (20)	---	+	---	---	---
3) 8S/25G (20)	---	+	---	---	---
4) 10S/25G (18)	---	+	---	+(2)	+(2)
5) 25S/25G (4)	---	---	+(2)	+(2)	---

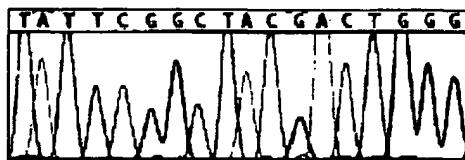
3S/25G



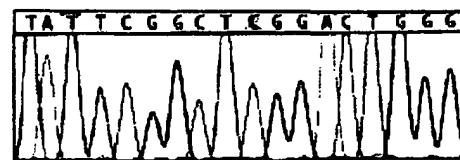
6S/25G



8S/25G



10S/25G



25S/25G



25S/25G

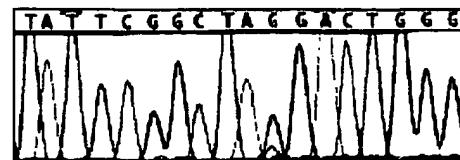
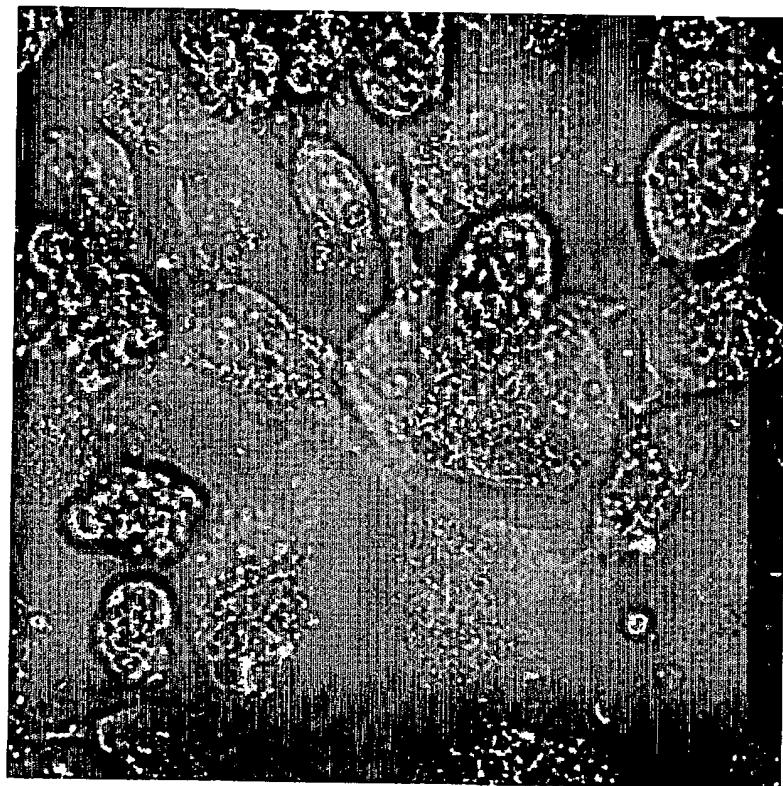
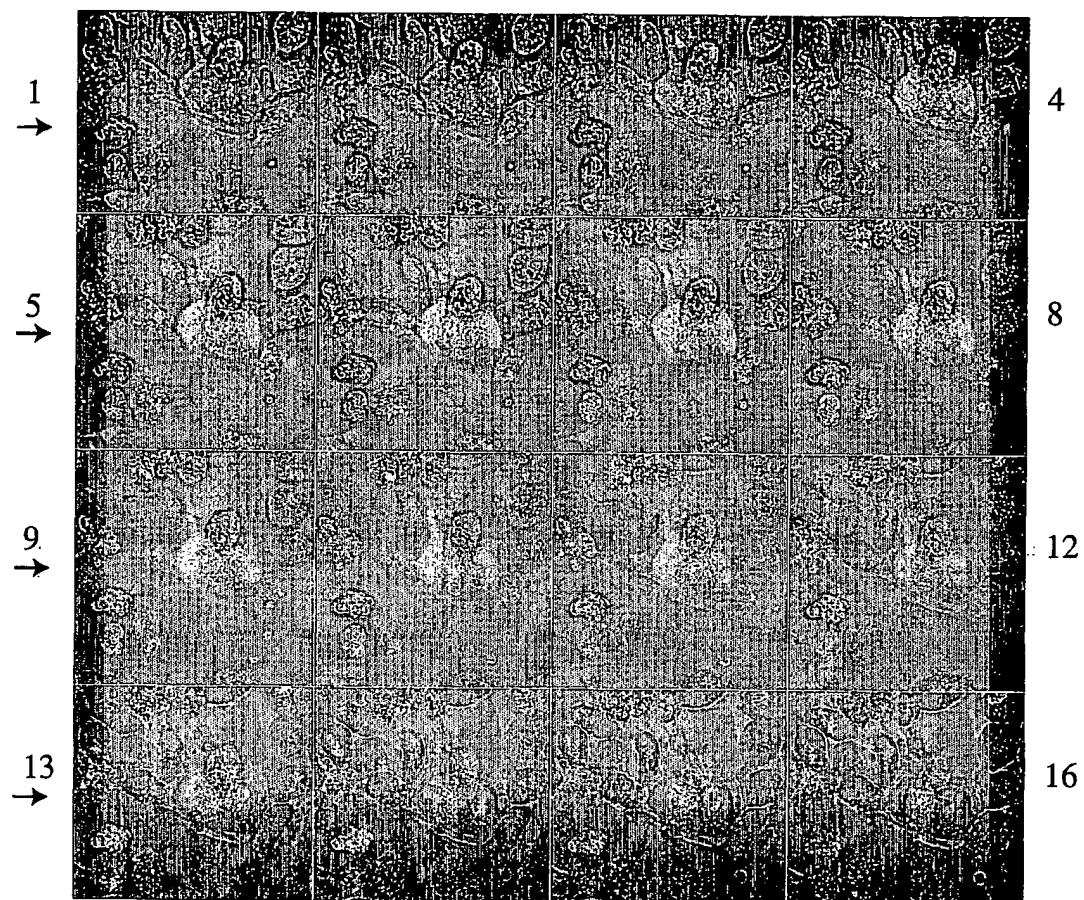


Figure 4



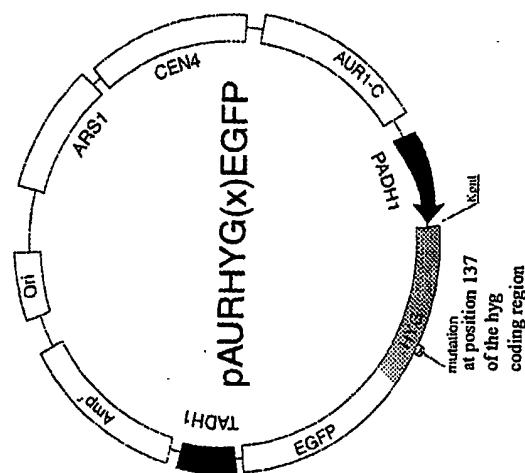
**Figure 5**



**Figure 6**

Sequence of normal allele: GTGGATAATGTCCCT  
 Target/existing mutant: GTGGATAAATGTCCCT  
 Desired alteration: GTGGATAACGTCCCT

Figure 7A



Sequence of normal allele: GTGGATAATGTCCCT  
 Target/existing mutant: GTGGATAAGGGTCCCT  
 Desired alteration: GTGGATAACGTCCCT

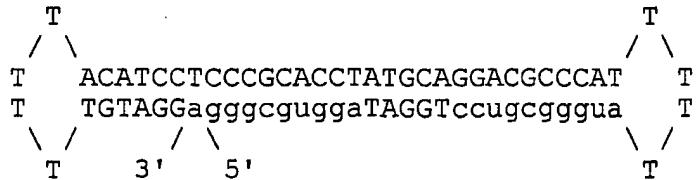
Figure 7B

HyqE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HyqE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC  
GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG  
CCG ATG GTT TCT AC-3'

HyqE3T/74α: 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG  
CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA  
GCT GAA AGC ACG AG-3'

HyqGG/Rev:



Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT  
CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG  
A-3'

Figure 8

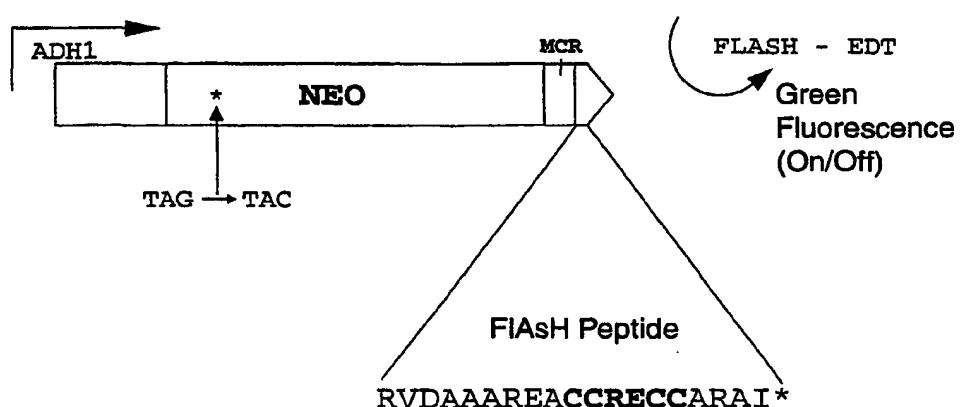
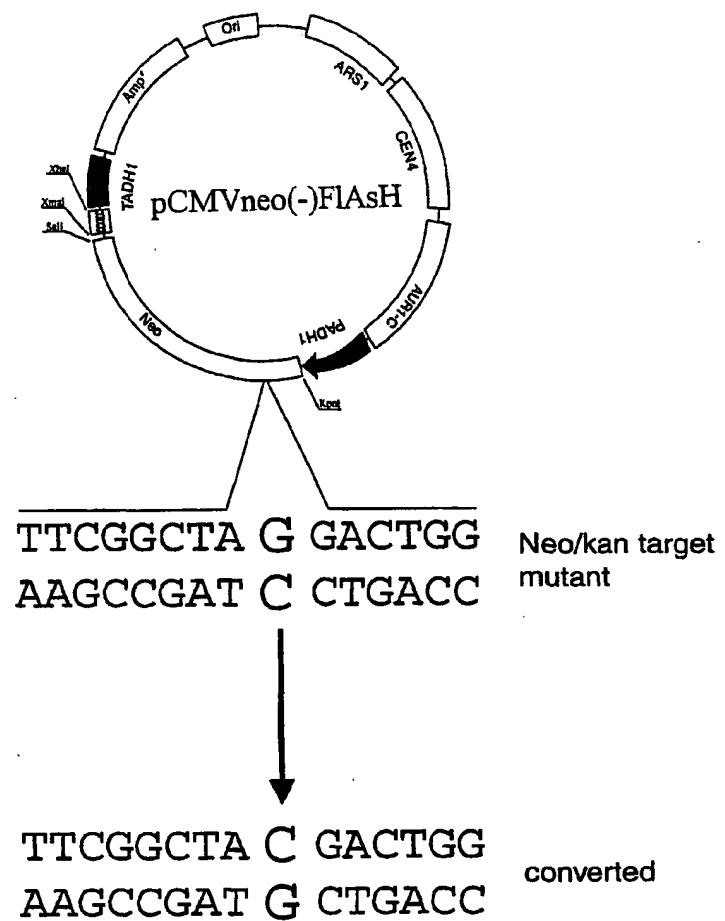


Figure 9

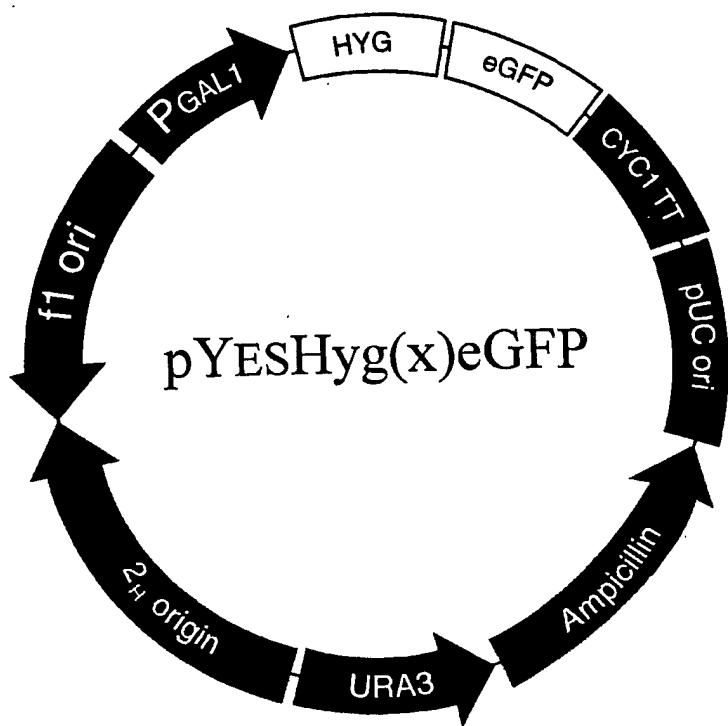


Figure 10

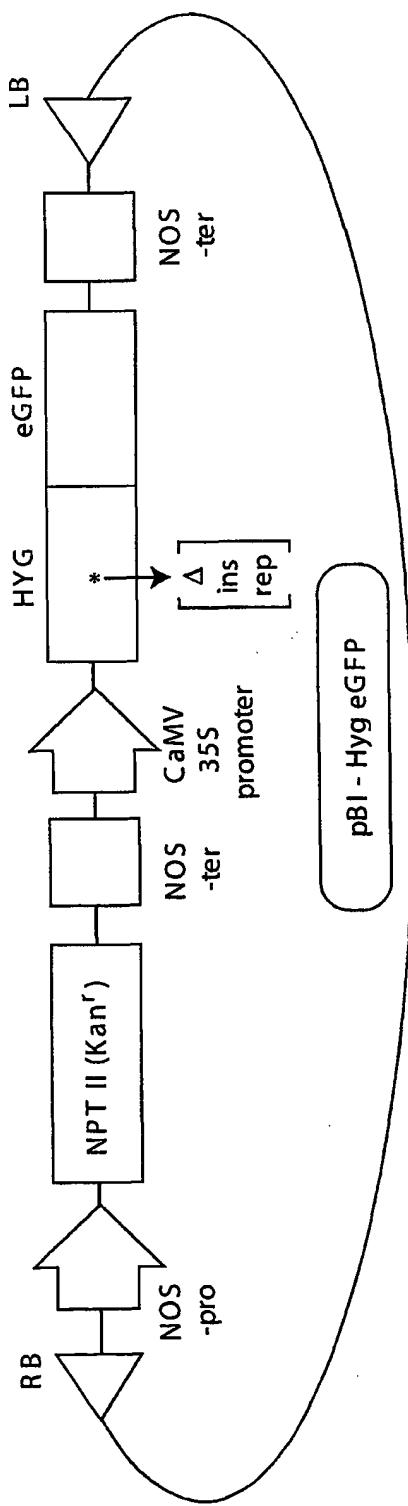


Figure 11